

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 33.3983 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWHULB-A
Perfect score: 5953
Sequence: 1 MALRVLLLTALTLCHGFNLD.....FKROYKDMSEGGPGAEPPQ 1153
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5953	100.0	1153	1 RWHULB	cell surface glyco
2	4542	76.3	1153	2 S00551	leukocyte surface
3	3510	59.0	1163	1 RWHULC	cell surface glyco
4	1556	26.1	1170	2 S03308	cell surface glyco
5	1546	26.0	1163	2 I56126	lymphocyte fuction
6	1160	19.5	1179	2 A53213	integrin alpha-1 c
7	1105.5	18.6	1151	2 A45226	integrin alpha-1 c
8	1096	18.4	1170	2 I45914	integrin alpha 2 s
9	1086	18.2	1178	2 S44142	VLA-2 protein homo
10	1084.5	18.2	1181	2 A33998	integrin alpha-2 c
11	1079	18.1	1180	2 A35854	integrin alpha-1 c
12	667	11.2	1039	2 A41131	lymphocyte-Peyer's
13	639	10.7	1038	2 S06046	integrin alpha-4 c
14	630	10.6	1035	2 I58409	integrin alpha-9 c
15	614.5	10.3	1041	2 T31437	integrin alpha cha
16	579.5	9.7	1054	2 J07294	alhap integrin -
17	573.5	9.6	1051	2 A35761	cell surface glyco
18	568.5	9.5	1053	2 I55534	VLA-3 alpha subuni
19	555.5	9.3	1053	2 S44250	integrin alpha-5 c
20	550	9.2	1034	2 A36108	integrin alpha-v c
21	533	9.0	1044	2 T10050	integrin alpha-v c
22	532	8.9	1049	2 A27079	fibronectin recept
23	532	8.9	1073	2 B36429	integrin alpha-6 c
24	529.5	8.9	1051	2 A40021	integrin alpha-3 c
25	528.5	8.9	1072	2 A38457	integrin alpha-6 c
26	525.5	8.8	1091	2 A15453	integrin alpha-6 c
27	524.5	8.8	1048	2 A27421	integrin alpha-5 c
28	517	8.7	1044	2 I56516	integrin alpha-8 c
29	506	8.5	1394	2 A29637	position-specific

30	496.5	8.3	1146	2 S40311	integrin - fruit f
31	495.5	8.3	1039	2 A34269	integrin alpha-2b
32	493.5	8.3	1037	2 A60163	glycoprotein IIB -
33	492	8.3	1137	2 JC5950	integrin alpha-7 c
34	488	8.2	1135	2 I61186	alpha-7 integrin -
35	486	8.2	126	2 B30892	leukocyte adhesion
36	474.5	8.0	1226	2 S44824	FS4r2.1 protein -
37	473	7.9	1106	2 S38783	integrin alpha cha
38	454.5	7.6	1139	2 S28277	hypothetical prote
39	452	7.6	1045	2 S60571	integrin alpha v c
40	433.5	7.3	1115	2 T09433	integrin alpha cha
41	426.5	7.2	1115	2 T09403	integrin alpha cha
42	391	6.6	764	2 I36916	glycoprotein IIB -
43	309	5.2	1086	2 T18523	integrin alpha cha
44	301.5	5.1	272	2 A55348	integrin alpha-1 -
45	299	5.0	604	2 I36917	glycoprotein IIB -

ALIGNMENTS

RESULT 1

RWHULB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11B).

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <COR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148

A>Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1.

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965,'P',967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594

A>Note: the authors translated the codon TAC for residue 1129 as Thr

A>Note: part of this sequence, including the amino end of the mature protein, was confir

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regu

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:8909893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

A>Note: part of this sequence was confirmed by protein sequencing
 R:Flaming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
 J. Immunol. 150, 480-490, 1993
 A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in
 n during evolution.
 A:Reference number: A46526; MUID:93123748; PMID:8419480
 A:Accession: A46526
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-499,501-1153 <FILE>
 A:CROSS-references: GB:SS2227; NID:9263047; PIDN:AAB24821.1; PID:9263049
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
 A>Note: sequence extracted from NCBI backbone (NCBI:121963)
 R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
 Biochim. Biophys. Acta 874, 368-371, 1986
 A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
 A:Reference number: A90664; MUID:87076671; PMID:3539202
 A:Accession: A26091
 A:Molecule type: protein
 A:Residues: 17-31 <PIE>
 A:Experimental source: granulocytes
 R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
 Blood 79, 865-870, 1992
 A>Title: Characterization of the myeloid-specific CD11b promoter.
 A:Reference number: 152567; MUID:92144986; PMID:1346576
 A:Accession: 152567
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:CROSS-references: GB:M84477; NID:9180184; PIDN:AAA51960.1; PID:9553219
 C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
 C:Genetics:
 A:Gene: GDB:ITGAM; CR3A
 A:CROSS-references: GDB:120599; OMIM:120980
 A:Map position: 16p11.2-16p11.2
 A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
 F:17-1108/Domain: extracellular #status predicted <EXT>
 F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:465-473/Region: calcium/magnesium binding #status predicted
 F:530-538/Region: calcium/magnesium binding #status predicted
 F:593-601/Region: calcium/magnesium binding #status predicted
 F:1109-1134/Domain: transmembrane #status predicted <TM>
 F:1135-1153/Domain: intracellular #status predicted <INT>
 F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 100.0%; Score 5953; DB 1; Length 1153;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRVLLTALTLCGFLNLDTENAMTFOENARGFQGVVQSGRVVVGAPQEIIVANQR 60
 DB 1 MALRVLLTALTLCGFLNLDTENAMTFOENARGFQGVVQSGRVVVGAPQEIIVANQR 60
 QY 61 GSLVQCDYSTGSCPIRLQVPVEANVMSIGLSLAATTSPQLACGPTVHTCSENTYVK 120
 DB 61 GSLVQCDYSTGSCPIRLQVPVEANVMSIGLSLAATTSPQLACGPTVHTCSENTYVK 120
 QY 121 GLCFLFGSLNRQQQPKFPFALRGCPQEDSDIAFLIDGSGSIIPHDFRMKFVSTVMEQL 180
 DB 121 GLCFLFGSLNRQQQPKFPFALRGCPQEDSDIAFLIDGSGSIIPHDFRMKFVSTVMEQL 180
 QY 181 KSKTFLSLMQSEEFRIHFTFKFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFN 240
 DB 181 KSKTFLSLMQSEEFRIHFTFKFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFN 240
 QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300
 DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300

RESULT 2
 S00551

leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alpha chain

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S00551; I59078

R:Pytela, R.

EMBO J. 7, 1371-1378, 1988

A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir

A:Reference number: S00551; MUID:88312584; PMID:3044779

A:Accession: S00551

Matches 409; Conservative 211; Mismatches 464; Indels 110; Gaps 38;	
Qy	6 LLLTALTLCHEG-----NLDTENAMTFQ--ENARGFGQSVVQLQSGRVVVGAPQEI 54
Db	6 ITVMAMALLSGFFFPAPASSYNLDVRGASFSPPRAGRHFGYRVLQV-GNGVIVGAPGE- 63
Qy	55 VAANQRGSLYQCDYSTGCEPIRLQVPVBAVNMISGLSLAANTSPOLLACQPTVHQTC 114
Db	64 --GNSTGSLYQCGSGTGHCLPVTLR--GSNYTSKYLGMTLATDPTDGSILACDGLSRTCD 120
Qy	115 ENTYYKGLCLFLGSLNR-----QOPKFPEALRGCEQEDSIAFLIDGSGSIIPHDPFRMK 170
Db	121 QNTYISGLCYLFRQNLQGMLOQRFQECIKG-----NVDVLFPGSMISQDFBQKIL 176
Qy	171 EFVSTVMEQLKSKTFLSLMQTSEBFRIHFTFKFQNNPNRSLVKPIPTQLLGRTHRTATG 230
Db	177 DPMKDVMMKLSNTSYQFAAVQFSTSYKTEFDSYVKKWDPDALLKHVKHMLLINTFGA 236
Qy	231 IRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYEDVITPEADREGVIYVIGVGDA 290
Db	237 INYVATEVFREELGARPDATKVLIIITDGE--ATDSGNIDAADK-----IIRYIIGIKH 289
Qy	291 PRESEKRSQRLNTIAKPPRDHVFQVNNREALKTIQNOLREKXFALEGTQSGSSFEHEM 350
Db	290 FTKESQETLHFPASKPASEFVKILDTFEKLDLFTTELQKKIYVIEGTSKQDLTSFNMEL 349
Qy	351 SOEGFSAITSGPLLSTVSGSDWAGGVP-LYTSKEKSTFINMTRVDSMDNDAYLGYAAA 409
Db	350 SSSGISADLSRGHAVVGAGKADWAGGFLDLKADLQDDTFIGNEPLTPEVRAGLYGTYT 409
Qy	410 -IILNRVQSLVLGAPRYOHIGLVAMFR--QNTGMWESNANVKYQIGAYFGASLCSVDV 466
Db	410 WLPSRQKTSLLASGAPRYOHMGRVLLFQBPQGGHWSQVQTHGTQIGSYFGGELCGVDV 469
Qy	467 DSGNSTDLVLIGAPHYETRGQSVSVCLPRGORARWQCDV--LYCEQOGOPWRFGAA 524
Db	470 DQDGETELLIGAPLIFYGEGRGVFIY-----QRRQLGFEESVSELQGGPGPLGRFGGA 524
Qy	525 LTVLGDVNGDKLTVDAIGAPGEDNRGAVYLPFGHTSGSGISPSHSQIRAGSKLSPLQV 584
Db	525 ITALTDINGDLVDVAVGAPLEE--QGAVYIINGRHG-GLSQPQQRIBGTQVLSGIQWF 581
Qy	585 GOSLGGQDLTWGDLVLTGAGHVLLRLRSQVPLRVKAIMFENPREVARNVFCNDQV 644
Db	582 CRSIRGVKDLGDLGADVAVGAESQIVLSSRPVDMVTLMSPSPAEIPVHEVECSYSTS 641
Qy	645 -KGKEAGEVRVCLHVQKSRRDLRGOIQSVTYDLALDSGRPHSRVNETKNSTRQT 703
Db	642 NQKKEGVNITICQI-KSLYQF-QGRLVANUTYTLQLDGHRTRRRGLPFGGRHELRRNI 699
Qy	704 QVLGLTQTCETLKLQLPNCIEDPVSPIVLRNFSL---VGTPLS--AFGN-----LRPVL 753
Db	700 AVT-TSMSCDTDFSFPFVCVDLIISPINVSINFLSWEEBGTPRDQRAQGDPIPLRPSL 758
Qy	754 ABDAQRLFTALPPFKNCNDNIQDDLSITFSFMSLCLVVGGRPFNVTVTVRNDEG 813
Db	759 HSETWEI-----PFEEKNCDEKCEANLRVSPSPARSRALRTAFASLSVELSLNLEED 813
Qy	814 SVRTQVTPFFPLDLSVRKYSTLQNRQSQRSLACES--ASSTEVSGALKSTSCSINHPI 871
Db	814 AYVQDLHLFPGLSFRKVEML---KPHSQIIPVSCBELPEERLLSRAL---SCNVSGPI 867
Qy	872 FPENSEVTFNITFDVDSKASLGKLLKANVTSENN---MPRTNKTEFQLELPVKYAVY 927
Db	868 FRAGHSVALQMMFNTLVNSSWGDSEVELHANVTENNEDSLLEDNATTI---IPILYPIN 924
Qy	928 MVVTSHGVTSTKYNFTASENTSRVMOHQVQV---SNLGORSIP-LSLVLPLVPRLNQTVI 983
Db	925 ILIQQEDSTLVSETPKPKIHQVKHMYQVRIQPSIHDHNIPTLEAVGVGPQPSSEGP 984
Qy	984 WDRPOVTVSENLSSCTCHTK--BRLPSHSD--FLAELRKAPVNVNCSTAVCQRQCQDIPFG 1039
Db	985 THQWSQVMEPPV--PCHVEDLERLDAAEPCPLGALFRCPFV-----1024

Qy	1040 IOEEFNATLKGNSLFDWIKTSHNHLIVSTAEILFNDSVFTLLPCQGFVARSQETKVE 1099
Db	1025 PRQEILVQVIGTLELVGREIAS-SMFSLCSLSISFNSKPHLYGSNASL-AQVVMKVD 1082
Qy	1100 PREVNPIPLIVGSSVGGLLLLALATAALYKLGFFKQKQKQKMMSEG-GPPGABP 1152
Db	1083 VYBERQMLYLYLSGIGGILLLLFIYLVYKVGFFKRNLERKMEAGRPVNGIP 1136
RESULT 5	
156126	
Lymphocyte fuction-associated molecule-1-alpha - mouse	
C:Species: Mus musculus (house mouse)	
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004	
A:Accession: I56126	
R:Kaufmann, Y.; Tseng, E.; Springer, T.A.	
J. Immunol. 147, 369-374, 1991	
A:Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit at	
A:Reference number: I56126; MUID:91268576; PMID:2051027	
A:Accession: I56126	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1163 <RES>	
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786	
C:Genetics:	
A:Gene: LPA-1	
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol	
F:151-315/Domain: von Willebrand factor type A repeat homology <WVAL>	
Query Match 26.0%; Score 1546; DB 2; Length 1163;	
Best Local Similarity 34.1%; Pred. No. 1.5e-97;	
Matches 408; Conservative 217; Mismatches 464; Indels 106; Gaps 38;	
Qy	1 MALRV-----LLLTALT-----CHGFNLDTENAMTFQENA-RGFGQSVVQLQSGRVVVGAPQ 52
Db	1 MSFRAGPRLLLGLQLFQAKWSYNLDRPTQSLAQAGRHFGYQVLQIEDG-VVVGAPG 59
Qy	53 EIVAAQRGSLYQCDYSTGSCPIRLQVPEVAVNMISGLSLAATTSPOLLACGPTVHOT 112
Db	60 E---GDNTGGLYHCTSSSEFCQPVSLH-GSNHTSKYLGMTLATDAAGKLSLLACDGLSRT 115
Qy	113 CSENTYVKGCLPFGSNLRQQPKFPEALRGCPQSDSDIAFLIDGSGSIIPHDFRMKGF 172
Db	116 CDQNTYLSGLCYLFPQSLGEPMLQNRPAYQECMKGKVDLVFLFDGQSGLDRKDFEILEF 175
Qy	173 VSTWMEQLKSKTFLSLMQYSEEPRIHFTFKEF-QNNPNRSLVKRPIPTOLLGRTHATGI 231
Db	176 MKDVNRKLSNTSYQFAAVQFSTDCRTEFTFLDYVQKNRNPVDVLLGSGVQPMFLLTNTFRAI 235
Qy	232 RKVRELFNITNGARKNAFKILVITDGEKFGDPLGYEDVIVEADREG-----VIRVY 284
Db	236 NYVVAHVFEESGARPDATKVLVIITDG-----EASDKGNISAAHDITRYI 281
Qy	285 IGVGDAFSEKRSQBELNTIASPPRDHVPQVNNFSAKTIQNOLREKXFAIBGTQTGSSS 344
Db	282 IGIGKHFFVSQKQKTLHIPASEPVEEFVKILDTFEKLDLTDLQRRIVAIEGTNRQDLT 341
Qy	345 SPEHEMSQEGFSAAITSNGPPLLSTVSGVDWAGGVP-LYTSKEKSTFINMTRVDSMDNDAY 403
Db	342 SFNMELSSSGISADLSKGHAVVGAGKADWAGGFLDLREDLQCATVFGQEPLTSDVRGGY 401
Qy	404 LQYAAA-IILNRVQSLVLGAPRYOHIGLVAMFR--QNTGMWESNANVAGTQIGAYFGAS 460
Db	402 LGYTWAMTSSSRPPLAAGAPRYOHVGOVLFLQAPAEAGRRWNQTKIEGTQIGSYFGGE 461
Qy	461 LCSVDVDNNGSTDLVLIGAPHYETRGQSVSVCLPRGORARWQCDVAVLYGEQGPWGR 520
Db	462 LCSVDLDQDGAELLIGAPLFFGEGRGVFTY---QRRQSLFEMVSELQGDPPGPLGR 518
Qy	521 FGAALTVLGDVNGDKLTVAVTGAECEDNRGAVYLPFGHTSGSGISPSHSQIRAGSKLSPR 580
Db	519 FGAALTALTDINGDLRDLTVAVGAPLEE--QGAVYIINGKPG-GLSPQPSQRIQGAQVFPFG 575

Db 1073 SWD-----HSEELLKDVTELLQILGEISFNKSLYEGLNAENH--RTKITVTVFLDKERYHS 1112

Qy 1107 LPIIVGSSVGGLLLLALITALYAKLGFKKQYKDMMSGE 1144
||: |||||: | : |||||: | :
Db 1125 LPIIINKSVGGLLAVILVILFKCGFFKKRYQQQLNLE 1162

RESULT 7
A45226
integrin alpha-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45226
R;Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A:A>Title: Expression of native and truncated forms of the human integrin alpha 1
A:Reference number: A45226; MUID:93155124; PMID:8428973
A:Accession: A45226
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1151

A:Cross-references: UNIPROT:P56199
A:Experimental source: hepatoblastoma cell line HepG2
A>Note: sequence extracted from NCBI backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <WVAL>

Query Match 18.6%; Score 1105.5; DB 2; Length 1151;
Best Local Similarity 27.9%; Pred. No. 2.7e-67;
Matches 345; Conservative 211; Mismatches 486; Indels 195; Gaps 44

Qy 17 FNLDTENAMTFQENARG-FGGSVVQL---QGSRVVVGAPQEIVAANORGSIYQCDSYSGS 72
||: |||||: ||: |||||: ||: |||||: ||: |||||: ||:
Db 1 FNV DVKNSTMFSGPVEDMFGVTVOQYENEKGKWVLIGSPLVGPQKNRTGDVYKCPVGGRGE 60

Qy 73 CEP-IRLOVPVEA-----VNMSLGLSLAATTSPPQLLACGTPTHQTCSENTYYKGL 122
||: |||||: |||||: |||||: |||||: |||||: |||||: ||:

Db 61 SLPCVKLDELPTNTSIPNWTEVKENMTFGSTL-VTNPNGGFLACGPLVAIRCGLHLHTTGI 119

Qy 123 CFLFGSNLRQOPKFPEALRGCPQEDSDIAFLIDGSGSIIPHDPFRMKFEFYSTVMEQLK- 181
||: |||||: |||||: |||||: |||||: |||||: |||||: ||:

Db 120 CSDVSPTFOVNSIAP--VQECSTQ-LDIVIVLGSNSIYPWD--SVTAFLDLLKKRMDI 174

Qy 182 -KSKTLPSLMQYSEEPRIHFTFEKFPNNPRSLVKPIITOLLGR-THTATGIRKVVRELF 239
||: |||||: |||||: |||||: |||||: |||||: |||||: ||:

Db 175 GPQQTGVIVOYGENVTHFNLNKYSSTEELVAACKIVQGGRGQTMTALTGDTARKEAF 234

Qy 240 NITNGARKNAFKILVLTDEKFGDPLGYEDVIPEADREGVIRVIVGVGDAFR-----SE 294
||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 235 TEARGARRGVKKVMVITVDGESH-DNHRLKKVIQDCDENIQRFSAILGSYNRGNJTSE 293

Qy 295 KSRQELNTIASKPDRDHVFVNNEPALKTINQLRKXFALEGTTQGTGSSSFHEMSOEG 354
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 294 KFVEEIKSIASEPTEKHFFNVSDDELAVTIKTERIFALEANTDAQSAASFEMMSQTG 353

Qy 355 FSAAITSNGLLSTVSGYSWAGGVFLYTSKE-----KSTP-INMTRVDSNDNDAYLYGAA 408
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 354 FSAHYSQDWMLGAVGAYDNMGTVVMOKASQIIIPRNTPNFVESTKKNLEPL-ASYLGYTV 412

Qy 409 AIILNRVQS-LVGAPRYQHIGLVAMPFRQNTGWESNANKVGTQIGAYFGASLCSDVD 467
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 413 NSATASSGDVLYTAGQPRYNHTGVIIYRMBDGNIKILTLLSGEQIGSYFGSIILTTDD 472

Qy 468 SNGSTDVLVIGAPHY-----YEQTR-GGOVSVCLPRQQRARWCDAVLY 511
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 473 KDSENTDLLGAPNMGMTEKEEQKVYVYALNQIRFYQMSELEFIKQTCSSRQUNSCCTT 532

Qy 512 GEOQPWG-RFGAALTVLGDVNGDKLTDVAITGAPCEEDNRNAVLYFHGTSGSGISPSSHQ 570
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 533 ENKNIEPCGARFGTAIAAVKDNLNDGFDNIVIGAPLEDHDGGAUVIYHG-SGKTIRKEYAQ 591

Qy 571 RIAGSKLSPLOYPGQSLSGQDLTMGLVDLTVGAQGHVLLLRSQPVLRVKAIIMEFNPR 630
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

Db 592 RIPSGDGKTLKPFQSGIHGEMDLNGDGLTDVTIIGLGGAALFWSRDVAVKVTMNFPFN 651
||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:

```
Db 133 YTTGCVSDVSPDF-QRTSFAPAVQCP-SFIDVVVVCDSESNISYPWD--AVKNFLEKVF 188
QY 178 EQLK--KSKTLFSLMOYSEPRHFHFFKEFQNNPNSRLVKPIITOLL-----GRTHATGCI 231
Db 189 QGLDGTPTQWGLQYANNPRVFNLTFSKSD---EMIKATSTQFYGGDLTNTFFKAI 245
QY 232 RKVRELFINITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRVIGV----287
Db 246 QYARDTAYSTAAGRGATKVMVWVTDGESH-DGSKLKAVIDQCNDNLRFGLVGLYL 304
QY 288 -GDAPRSEKRSQELNTIASKPRDRHVQVNNFEALQIONQRKXPAIEGTQTGSSSF 346
Db 305 NNALDITKNLKEIKAIASIPTRHFNFVDSBADLLEKAGTIGEOIFSIEGVQVQ-GDNF 363
QY 347 EHEMSQEGFSAIT--SNGPLISTVGSYDWAGGVLYTSKESKSTFINMT--RVDSDMN-D 401
Db 364 QNEMQVQFSAEYSQNNILMGAAYDWSVTVQKTPHGHILIFSQAFOEILQDRHS 423
QY 402 AYLGVAAAILLRNVQSLVLGAPRYOHIGLVAMFRQNTGMWESNANV-----KGTQIGA 455
Db 424 SYLGYSVASISTGNSVHFVAGAPRANYTGOIVLYSVN-----ENGNTVVIQSGRDQIGS 478
QY 456 YFGASICSVDVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCLPRQQRARWCCDAVLIGE 513
Db 479 YFGSVLCADVNNKDTITDVLVGAPMYNDLKEEGRVLYFTITKG-ILNMH--OFLRGP 535
QY 514 QQQPGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVLPHGTSGSGISPSHSORIA 573
Db 536 NGLNARFGSAALSDINWDGFNDVIVGSPLENQSGAVIYNGHEGM-ILRYSQKIL 594
QY 574 GS--KLSRPLQVFGSLGSGQDLTWDGLVDLVGAGHVLRLRSQPLVRKVAIMEFNPRE 631
Db 595 GSDRAFSSHLQYFGRSLDYGDLNGDSITDVSAGAFQVQVQLWSQSIAVDSVDSFTPKK 654
QY 632 VARNVFECDQVVKKEAGEVCLHVQKSPDRLEGOIQSVVYTDLALD-----SGRPH 687
Db 655 I--TLNKNAEI-----KLKCF-----SAKFRPTNQNNQVAVIYNTITDEQSSRVI 701
QY 688 SRAVENETKNSRRQTQVLGLTQTCF--TLKLQPLNCIEDPVSPIVLRNLSL--VGRPL 743
Db 702 SRGLFKENNERCLQKTMIVSQARCSSEYIIHQEPS---DIISPLNLCWNISLENPGT--756
QY 744 SAFGNLRPVLABDAQRFTALPFFKNCNGNNICDDLSITF-----SPMSLDCLVVGGR 799
Db 757 -----NPALEAYSETVVFSPFHKCGDGDGVCISDLVNLVQLPATQQPFFIVSNQNK 810
QY 800 EPNVTVVRNDCEDSVRTQVTFRPLDLSYRKVSTLQNRQSRWRLACESASST-EVSG 858
Db 811 RLTFVQLANKKESAYNTEIVVDFSENLF-----ASWMPVDGTGTEVTCQIAS 858
QY 859 ALKSTCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRTNKTPEQL 918
Db 859 SQKSVTCNVGYPALKSKQVQVTFINFDNLQ-NLQNASISFRALSESQENWADNSVNL 917
QY 919 ELPVKAYVMVTSIGVSTKYNLFTASNTSRVMOHQVQVNLQOR-----SLPI 968
Db 918 KLSLLYDAEIIHT-RSTNINFEVSLDGNVSSV-HSFE--DIGKPTFSIKVTIGSVVP 973
QY 969 SLVFLVPVRLNQTIVLWRPQVTFSEN--LSTCHTKE-----RLPSHS 1009
Db 974 SWA-----SVIIHPQYTKDKNPLMYLTVGHTDQAGDISCEAEINPLKIGQTSVV 1024
QY 1010 DFLAF-LRKAPVYNGSIAVCORIQCDIPFGTQEEFNATLKNLSFDWYIKTSHNHLIV 1068
Db 1025 SFKSENFRIKELNCRATSCNIMCWLADLVQKGEYFLNVSTRWNGTFAASTQTQVLT 1084
QY 1069 STAEI-LFNDSVFTL-----LPGQAFVRSQETKVEPFE-VNPNPLVIGSSVGGILL 1120
Db 1085 AAAEIDTNPQIYIETENVITIP-----LTIMKPEKVEYPTGIVGSIAGILL 1134
QY 1121 LALITAAALYKLGFFKRYQKDM 1141
Db 1135 LLALVAILWKLGFKKRYEKM 1155
```

RESULT 9

S44142

VLA-2 protein homolog - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S44142

R:Edelman, J.M.; Chan, B.M.; Uniya, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latzei;

submitted to the EMBL Data Library, January 1994

A:Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not

A:Reference number: S44142

A:Accession: S44142

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1178 <DE>

A:Cross-references: UNIPROT:Q62469; EMBL:Z29987; NID:G473098; PID:CA82877.1; PID:G47305

F:169-344/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match

Best Local Similarity 18.2%; Score 1086; DB 2; Length 1178;

Matches 347; Conservative 210; Mismatches 492; Indels 188; Gaps 44;

QY 5 VLLTALTLCGPNLDTENAMTFQ-ENARFGQSVVQL---QGSRVVVGAPQEIIVANQR 60

Db 15 LMLVQGLNCLAYNVGLPGAKIFSGPSSEQFGYSVQQLTNPQGNWLLVGSWSPGFPEPRM 74

QY 61 GSLYQC--DYSTGSCPEIRLQ-----VPEAVNMSLGLSLAATSPPOLLAGCPVHQ 111

Db 75 GDVYKCPVDLPTATCEKLNQNSASISNVTBIKTNMSLGLTLTRNPGTGGFLTCPLWAH 134

QY 112 TCSENTYVKGICFLFGSNLRQPPQ---KFPALRGCPQEDSDIAFLIDGSGSIIPHDPFR 168

Db 135 QCGNQYATGIC---SDVSPDFQFLTSFSAVQAACPSL-VDVVVVCDESNIYP--WEA 187

QY 169 MKEFVSTVMEOLK--KSKTLFSLMOYSEPRHFHFFKEFQNNPNSRLVKPIITQLLQ-RT 225

Db 188 VKNELVFTGLDITGPKKTKVALLQYANEPRIIFNLNDFETKEDVMQVATSETRQHGDLT 247

QY 226 HTATGIRKVVRELNITNGARKNAFKILVITDCEKFGDPLGYEDVPEADREGVIRVI 285

Db 248 NTFRAIFARDYAYSQTSGGRPATKVMVVVTDGESH-DGSKLTVIQQCNDDBILRPGI 306

QY 286 GV-----GDAPRSEKRSQELNTIASKPRDRHVQVNNFEALQIONQRKXKFAIEGTQT 340

Db 307 AVLGLNRLNALTKNLKEIKAIASITPTERYFFNVADAELAKETLGEQIFSEGTQV 366

QY 341 GSSSPFHEMSQEGFSA--ALTSNGPLLSVTSVGDWAGGVLYTSKESKSTFINMT--RVD 396

Db 367 G-GDNFQWMAVQVGSADYAPQNDILMLGAVGAFDWSGTLVQETSHKRPVIPPQAFDQVL 425

QY 397 SDMN-DAVLGYAAAIILNRNVQSLVLAQPRVHOHIGLVAMPQNTGMWESNANV---KGT 451

Db 426 QDRNHSFLGYSVAIAISTEDGVHFAVAPRANYTGOIVLYSVNK---QGNVTVIQSHRGD 482

QY 452 QIGAYFGASCLSDVDVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCLPRQQRARWCCDAV 509

Db 483 QIGSYFGSVLCSVDVDKDTITDVLVGAPTYMNDLKEEGKVLFTITKGLNQHQ---F 539

QY 510 LYBQGGQPGWRFGAALTVLGVNGDKLTDVAIGAPGEDNRGAVLPHGTSGSGISPSHS 569

Db 540 LEGPEGTGNARFGSAIALSDINMDGFNDVIVGSPVENENSGAVIYNGHQGT-IRTKYS 598

QY 570 QRIAGSKLSR--LQYFGQSLSGQDLTMDGLVDLTVGAQGHVLLRSQPLVRKVAIMEF 627

Db 599 QKILGSGNARFRHLQFFGRSLDYGDLNGDSITDVSIGALGQVQLWSQSIAVDAIALP 658

QY 628 NPFEARNVFECDQVVKKEAGEVRLVQKSTRDLREGQIQSVVYTDLALD-----S 683

Db 659 TP-----DKITLLNKDAKITLCLCFRAEFEPAGQNNQV--AILENMTLDADGHS 705

QY 684 GRPHSRAVFNETKNSRRQTQVGLTQTCF--LKLQPLNCIEDPVSPIVLRNLSLVTG 741

Db 706 SRVTRGVRENSEFLQKNMVVNEVQKSEHHISIQKPS-----DVVNELDLRVDISLNP 762
Qy 742 PLSAFGNLRPVLAEADAQRLFTALPFPERKNGNDNICQDDLSI-----TFSPMSLDC 792
Db 763 GTS-----PALEAYSETVKVPSIFPYKEGSGDGCISDLILDVQQLPAIQTSF-----811
Qy 793 LVVGGPRENVTVTVRNDEGSYRTQVTFPPPLDLSYRKVSTLQNRQSRWRLACESAS 852
Db 812 IVSNQNKRLTFSVILKNRGESAYNTVLAESFSENLF-----ASFSPVDGTE 859
Qy 853 ST-EVSGALKTSCSINPIPPENSEVTFNITFDVDSKASLGNKLLKANVTSENNMPT 911
Db 860 VTCEVGSQKSVTCVGVGYPALAKSEQVTFINFDNLQ-NLQQAANFQAFSEQ--ET 916
Qy 912 NKTE--FOLELPVKYAVVMVTVSHGVSTKYLNTASENTSRVMQHYQVSNLQGR-----964
Db 917 NKADNSVSLTIPLLYDAELHLT-RSTNINFYBISDENAPSVIK---SVEDIGPKPIFSL 972
Qy 965 -----SLPISLVFLV-----PVRLNQTVID 985
Db 973 KVTAGSAFVMAVTVIHPIQYTKRNPLLYLTGIQDQAGDISCTAEINPLKLPHTA---1029
Qy 986 RPQVTF-SENLSTCHTKERLPSHDSFLAELRKAPVWNCIAVCQRIQCDIPFFGIGEEF 1044
Db 1030 -PSVSKNEFR---HTKE-----LDCRTTSCSNITCWLKDLHMKAY 1068
Qy 1045 NATLGNLSFQWYIKTSHNNHLLIVTAEILFENDSVFTLLPGQGAFAVRSQETKVPFPEVP 1104
Db 1069 FINVTVRNRTFAASTQTQVLTAAAEIDTHNPQLFVIEENAVTIPLMIMKPTKAEVP 1128
Qy 1105 NPLPIVGVSSVGLLLILALITAAALKLGFPRKQYKDM 1141
Db 1129 T--GVIIIGSIITAGILLAMTAGLWKLGFPRKQYKDM 1163
RESULT 10
A:33998
Integrin alpha-2 chain precursor - human
N:Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2 ch
C:Species: Homo sapiens (man)
C:Date: 30-Mar-1990 #sequence revision 18-Sep-1992 #text_change 09-Jul-2004
C:Accession: A33998; B56793; A53117
R:Takada, Y.; Hemler, M.E.
J. Cell Biol. 109, 397-407, 1989
A:Title: The primary structure of the VLA-2/collagen receptor alpha (2)-subunit (platelet
A:Reference number: A33998; PMID:89308879; PMID:2545729
A:Accession: A33998
A:Molecule type: mRNA
A:Residues: 1-1181 <TAK>
A:Cross-references: UNIPROT:P17301; GB:X17033; NID:G33906; PIDN:CAA34894.1; PID:G33907
A:Note: The authors translated the codon GAT for residue 802 as Gln, GTC for residue 803
R:Catimel, B.; Parmentier, S.; Leung, L.L.; McGregor, J.L.
Biochem. J. 279, 419-425, 1991
A:Title: Separation of important new platelet glycoproteins (GPIa, GPIC, GPIC*, GPIIa an
A:Reference number: A56793; PMID:92061944; PMID:1953640
A:Accession: B56793
A:Molecule type: protein
A:Residues: 30-43 <CAT>
A:Experimental source: platelet
R:Zutter, M.M.; Santoro, S.A.; Painter, A.S.; Tsung, Y.L.; Gafford, A.
J. Biol. Chem. 269, 463-469, 1994
A:Title: The human alpha-2 integrin gene promoter. Identification of positive and negati
A:Reference number: A53117; PMID:94103255; PMID:8276836
A:Accession: A53117
A:Molecule type: DNA
A:Residues: 1-16, 'V', 18-21 <ZUT>
A:Cross-references: GB:L24121; NID:9400342; PIDN:AAAL6619.2; PID:G4583535
A:Note: authors translated the codon GTA for residue 17 as Leu
C:Genes:
A:Gene: GDB:JTGA2; CD49B
A:Cross-references: GDB:128031; OMIM:192974
A:Map position: 5q11.1-5q11.2
C:Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-1133/Domain: extracellular #status predicted <EXT>
F:172-347/Domain: von Willebrand factor type A repeat homology <VMA2>
F:1134-1154/Domain: transmembrane #status predicted <TM>
F:1155-1181/Domain: intracellular #status predicted <CT>
F:1105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)

Query Match 18.2%; Score 1084.5; DB 2; Length 1181;
Best Local Similarity 27.2%; Pred. NO. 7.9e-66;
Matches 338; Conservative 215; Mismatches 498; Indels 193; Gaps 44;

Qy 3 LRVLLLTALT-----LCHGFNLDTENAMTFQ-ENARGFGQSVVOL---QGSRVVVGAQPE 53
Db 11 LPLLLLVALLSOGILNCCLAYNVGLPEAKIFGSPSEQFGYAVQQINPKNMLLVGSPPWS 70
Qy 54 IVAANQRGLSYQC--DYSTGCEPIRLQ-----VPVEAVNMSLGLSLAATTPSPQLLA 104
Db 71 GPPENRMGDVVKCPDVLSTATCEKLNLTSTISIPNVTEMKTNMSLGLILTRNMGTTGFLT 130
Qy 105 CGPTVHQTCSENTYKGLCFPLPGSNLRQOPKFPPEALRGCPQEDSDIAFLIDGSGSIIPH 164
Db 131 CGPLMAQQCGNQYTTGVCSDISPDF-QLSASFSPATQCPSSL-IDVVVVCDSESNISYWP 188
Qy 165 DFRMKFVSTVMEOLK--KSKTLFSLMOYSEERPHETFEFQNNPNRSLVVKPIQTOLL 222
Db 189 D--AVKNFLEKPVQGLDIPGKTQVGLIQYANNPRVFNLTNYTKKEMIVATSSQSG 246
Qy 223 G-RHTATGIRKVRKLEFNITNGARKNAFKILVITDGEKFDPLGYEDVIPEADREGVI 281
Db 247 GDLTNTFCAGIYQARYKAYSAASGGRRSATKVMVVVTDGESH-DGSMKAKAVIDQCHNDNL 305
Qy 282 RYVIGV-----GDAPRSEKSRQELNTIASKPRDHVFOVNNPEALKTTQONREKXFAIE 336
Db 306 RFGI AVLGNRNALDITKNLKEIKAIASIPTEYFFNVNDEAALLKAGTIGEIQFSIE 365
Qy 337 GTQTGSSSSFEHMSOEGFSAITSNP--LLSTVGSYDAGGVPLYSKESKSTFINMT- 393
Db 366 GTVQG-GDNFQEMSQVFSADYSQNDILMGA VAGFGMSGTIVQKTSHGHLIIPKQAF 424
Qy 394 -RVQSDMN-DAYLGYAAAIILNRNVQSLVLAGAPRYQHIGLVAMFRQNTGMMESNANV---448
Db 425 DQILDQRNHSVLYGYSVAISTGESTHFVAGAPRANYTGQIVLYSVN-----ENGNITVI 479
Qy 449 ---KGTQIGAYFGASLCSVDVDSNGSTDLVIGAPHYYEQTR--GGQVSVCPPLRGQAR 503
Db 480 QAHRGDQIGSYFGSVLCSDVDVDKDTITDVLVAGAPMYSDLKKEGRVYLFITIKGILCO 539
Qy 504 WQCDAVLYGEOGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVILFHTSGSG 563
Db 540 HQ---FLSGPGIEINTFRGSAALASDINMDGNDVI VGSPLNQNQSGAVIYINGHGT- 595
Qy 564 ISPSHSQRIAGS--KLSPRLQYFGQSLSGGQDLTMDGLVDTLVGAQGHVLLLSQPVLRV 621
Db 596 IRTKYSQKILSDGDAFRSHLYQFGSLDGYDGLNGSDITDVSIGAFGVVQLWSQSIADV 655
Qy 622 KAIMEFNPREAVNFECDNQVVKKEAGEVRVCLHVOKSTRDRLEGOIQSVTVYDLAL 681
Db 656 ATEASFTEPKI--TLVNKNAQII-----LKLCP-----SAKFRPTKQNNQVAIVNITL 702
Qy 682 D-----SGRPHSRAVENETKNSRRQTQVLGLTQTC--ETLKLQPLNCIEDPVPVILRLN 735
Db 703 DADGFSRVTSRGLFKPENNERCLQKNMVVNOAQSCPEHIYIQEFS---DVVNSDLRLVD 759
Qy 736 FSLVGTPLSAFGNLRFPVLAEDAQRLLFTALFPPEKCKGNDNICQDDLSITF-----SPMSLD 791
Db 760 ISLENPGTS-----PALEAYSETAKVFSIPHKCGEDGLCISDLVDLRQIPRAEQEP 813
Qy 792 CLVWGGPREFNVTVTVRNDEGSYRTQVTFPPPLDLSYRKVSTLQNRQSRWRLACESA 851
Db 814 FIVSNQNKRLTFSVTLKKNRESAYNTGIVVDPSENLFF-----ASFSLPVDGT 861
Qy 852 SST-EVSGALKTSCSINPIPPENSEVTFNITFDVDSKASLGNKLLKANVTSENNMPT 910

Db 862 EVTCQVAASQSVACDVGPALKRQVTFITNFNLQ-NLQNOASLSFQALSBSQEN 920
Qy 911 TNKTEFQLELPVKYAVVMVTSHTGVTSTYNTFASNTSRVMQHOYQVSNLQOR----- 964
Db 921 KADNLVNLKIPLYDAEI-----HLTRSTNINFEYISSDGNVPSIVHSFEDVGPKFIFSLK 976
Qy 965 ----SLPISLVFLV-----PVRNLQTVIWR 986
Db 977 VTTGSPVSMATVITHIPOYTKKNPLMYLTGVQTDKAGDISCNADINPLKIGQI-----S 1032
Qy 987 POVTF-SENLSSTCHTKERLPKSHDFLAELKAPVWNCISIAVCQRIQCDIPFGIQEFPN 1045
Db 1033 SSVSKSENFH-----HTKE-----LNCRTASCNVTCWLVDVHMKGEYF 1072
Qy 1046 ATLKGNLSPDWIKTSHNHLIVSTAEI-LFNDVSFTLLPGGAFVRSQTKVPEPFEVP 1104
Db 1073 VNVTRINNGTFASFTQVQLTAAEINTYINPEIYV-----EDNTVTIPLMIM 1122
Qy 1105 NP-----LP--LIVGSSVGGLLLLALITAALYKLGFFFRQYKDM 1141
Db 1123 KPDEKAEVPTGVIGSIITAGILLALLLVAAILKWLKGGFFKRYEKM 1166

RESULT 11
A35854
Integrin alpha-1 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
R:Accession: A35854; S11243
J. Rignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, J. Cell Biol. 111, 709-720, 1990
A:Title: Molecular cloning of the rat integrin alpha-1 subunit: a receptor for laminin A
A:Reference number: A35854; MUID:90338125; PMID:2380249
A:Accession: A35854
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1180 <IGN>
A:Cross-references: UNIPROT:P18614; GB:X52140; NID:G56493; PIDN:CAA36384.1; PID:G56494
C:Keywords: cell adhesion; cytoskeleton; transmembrane protein
F:170-345/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 18.1%; Score 1079; DB 2; Length 1180;
Best Local Similarity 27.6%; Pred. No. 1.9e-65;
Matches 350; Conservative 200; Mismatches 484; Indels 234; Gaps 47;

Qy 6 LLLTALTCHGNLTENAMTFQENARG-FCGSVQL-----QGSRVVVGAPQEIIVANQRG 61
Db 18 LTVILGFCVSNVDVKNMSFSGPVEDMFGYVQOYNEEGKWLIGSLPLVGQPKARTG 77
Qy 62 SLYQCDYSTGCEP-IRLQVPVEA-----VNMSLGLSLAATSPQLLACQPTVHQ 111
Db 78 DVMKCPVGRERAMPCKLDPNTSIPNVTEIKENWTFGSTL-VTPNPGGFLACGLYAY 136
Qy 112 TCSENTYVKGCLFGLSGLNRQOPKQFPALRGCPQEDSDIAFLIDGSGSIIPHDPFRMKE 171
Db 137 RCGHLHYTTGICSDVSPFTQVNVSPAP--VQBCSTQ-LDIVILVDGNSIYP--WESVIA 191
Qy 172 FVSTWMEQLK-KSKTSLMQLQSEFRHFTFKFQNNPRSLVKPIITQLLG-RHTHA 228
Db 192 FLNDLLKRMIDIGPKQTQGVQYGENVTHEFNLNKYSSTEEVLVAANKIGRQGLQMTA 251
Qy 229 TGIRKVVRELFNITGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRVIGVG 288
Db 252 LGIDTARKEAFTEARGARKVKVMVITDGEH-DNYRLKQVIOCDENIQRESIAL 310
Qy 289 DAFR-----SEKSRQELNTIASKPRDRHVQVNNFEALKTQNLQREKXFAIEGQTGSS 343
Db 311 GHYRNLSTKFEVBEIKSIASEPTEKHFNFVNSDELALVTIVKALGERIFALEATDQSA 370
Qy 344 SSFEHEMQEGFSAITNSGPLSTLVGSDVAGGVFLYTSKEKSTFINMT--RVDSDMND 401
Db 371 ASFEMESQTGFSAHYSQDVMVLGAVGYDMNGVTVMQKAMQMVIPHNTTFQTEPAQWNE 430

Qy 402 ---AYLGAAAIILNRNVQSLVGLGAPRYOHIGLVAMFRONTGMWESNANVKGTQIGAYFG 458
Db 431 PLASVLYGVNSATIPGDLVLIAGQPRYNHGVQVVIYKMGEDGNINILQTLGEGQIGSYFG 490
Qy 459 ASLCSVDVDSNGSTDLVLIGAPHY-----YEQTR-GGQVSVCPLPRGORA 502
Db 491 SVLTIDIDKDSYTDLLVAGAPMTMGTEKEBQGVVYVAVNQTRFQYQMSLEPIRQTCCS 550
Qy 503 RWQCDVLYGQGGOPWG-RFGAALTVLGDVNGDKLTVAIGAPGEEDNRGAVILPHFGTSG 561
Db 551 SLKONSCTKENKNEPCGARGFATAAANKDLNDFGVNDVVI GAPLEDDHAGAVIYHSG-SG 609
Qy 562 SGISPHSQRISAGSKLSRLQYFGQSLSGGQDLTMDGLVDTLTVGAQGHVLLRLRSQPLVR 621
Db 610 KTIIEAQAQIPSGDGDKTLAFGQSIHGEMDIANGDGLTDTVIGLGAALFWARDVAVV 669
Qy 622 KAIIEFNPREVARNVFECNDQVVGKEAG--EVRVCLHVQ-KSTRDRLRREGQIQSVVYTD 678
Db 670 KVTWNFEFNKYNIOKNCNR---VEGKETVCINATMCFHVLKSKEDSIYEADLQ----YR 722
Qy 679 LALDSGRPHSRVFNET-----KNSTRQTVLGLTQTCETLKLQLPNCI----- 723
Db 723 VTLDSLRQISRSFFSGTOERKIQRNITVRESE-----CIRHSFYMJDX 765
Qy 724 EDPVSPVILRLNFSILVGTPLSAFGNLRFLAEDAQRLFTALFPFEKNCNGNDNI CODDLSI 783
Db 766 HDFQDSVRVTLDFNLT-DPENG-----PVLDDALPNSVHEHI PPAKOCGNKERCISDLTL 819
Qy 784 TFSFMSLDCLVVGGPPE-FNVTVTNRDNGDSYQTTFPPPLDLVSYRKVSTLQNRQSR 842
Db 820 NVSTTEKSLLVKSGHDKFNKSVLTQKNGDSAYNTRTVVQHSPLNLFSGIBEIOKD---- 875
Qy 843 SWRLACSSASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLL-LKAN 901
Db 876 ----SCSN-----QNTICRVGPFPLRAGTVPFKIIFQNTSHLSNALIHLSAT 922
Qy 902 VTSNNMPRTNKTEFQLELPVKYAV---YMVVTSHGVS-----KYLNFASNTSR 950
Db 923 SDSEEPLESNDNEVNISIPVKYEVGLQFYSSASEHHISVAANETIPEFINST--EDIGN 980
Qy 951 VMQHQYQVSNLQGRSLP---ISLVF-----LVPVRLNQTVIWD-----RP--- 987
Db 981 EINVFTYIRKRGHPMPPELQLSISFPNLTADGYPLVPIG-----WSSSDNVNCRPSL 1034
Qy 988 -----OVTFES-----ENLSSTCHTKERLPKSHDFLAELKAPVWNCSTAV 1027
Db 1035 EDPFGINSKKWTISKSEVLKRGTIQDCSSTC-----GVATTCSLLP 1077
Qy 1028 CQRIQCDI-----PFFGIQIEF---NATLKNLSFDWIYIKTSHNHLIVSTAEILFND 1078
Db 1078 SDSLQVNVVLLLWKPTF-IRAHFSSLLNLTARGELK-----SENSSLTSSN----- 1123
Qy 1079 VPTLLPGGAFVRSQTKVPEPFPNPLP--IVGSSVGGILLILALITAYLKLGFPRK 1136
Db 1124 -----RKELAIQISKDGLPGRVPLVILLSAFAGLILLMLLILALWKIGFPRK 1172
Qy 1137 QYKDMWSE 1144
Db 1173 PLKKKMEK 1180

RESULT 12

A41131

Lymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse

N:Alternate names: integrin alpha-4

C:Species: Mus musculus (house mouse)

C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C:Accession: A41131; S16742

R:Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzmann, B.; Weissman, I.L.

J. Cell Biol. 115, 1149-1158, 1991

A:Title: Cloning and expression of cDNAs for the alpha subunit of the murine lymphocyte-

A:Reference number: A41131; MUID:92064645; PMID:1840602

A:Accession: A41131

QY 854 TEVSGALSKTSCSINHPIPPENSEVTNFTFDVDSKASLGNKLLKANVTSENNMPRTNK 913
Db 702 DFL-----KCSVGFPPMRKSKVEFSVIFDTSLS--GEEVLSFIVTAQSG--NTER 750
QY 914 TE-----FQLELPPVKYAVVMVTS-----HGVSTKYLNTASENTS---RVMQHOY 956
Db 751 SSLLHNTLVLMVPLMHEVDTGITGMSPTS FVYGESVDAANFIQLDDLECHFPQINITL 810
QY 957 QVSNLQORSPLSLVFL-VPVRLN-----QTVIWRDPQVTFSENLSSSTCHTKER 1004
Db 811 QVYNTGPSLPGSSVSIISFPNLSGGAEMFHVQEMVQGEKNGCSFQKQPTPCIIQBQ 870
QY 1005 LPSHSDFLAELRKA-----PVNCSIAVCORIQCDDIPFGIOEENATLKNLSFD 1055
Db 871 ENIFHTIFAFTKSGRKVLDCPKGISCULTAHN-----PSALAKESRTI-----D 917
QY 1056 WYIKTSHNHLIVSTAEILFNDSVFTLLPGQAFVRSQETKEP----- 1100
Db 918 IV-----MLNT-EILKDSVVQ-----FMSRAKVVDPAALRVETAHGNPEEV 962
QY 1101 ---FEVFN---ELPLIVG-----SSVGGILLALITAALYKLGFFKQYKDM 1142
Db 963 TVVFEALHNLPRGYVGVGIIAISLLVGLILFLLAVLLMKMGFFRRRYKEII 1015

RESULT 15
T31437
Integrin alpha chain SU2 - sea urchin (Lytechinus variegatus)
C:Species: Lytechinus variegatus (variegatus urchin)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31437
R:Hertzler, P.L.; McClay, D.R.
A:Submitted to the EMBL Data Library, May 1998
A:Description: The EMBL SU2, a sea urchin integrin which binds laminin.
A:Reference number: Z12035
A:Accession: T31437
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1041 <HR>
A:Cross-references: UNIPROT:076378; EMBL:AF067658; NID:g3220240; PID:g3220241; PIDN:AACZ
A:Experimental source: developmental stage embryo
C:Function: binds laminin
A:Description: binds laminin
C:Superfamily: integrin alpha-2b chain

Query Match 10.3%; Score 614.5; DB 2; Length 1041;
Best Local Similarity 24.8%; Pred. No. 1.3e-33;
Matches 236; Conservative 155; Mismatches 314; Indels 245; Gaps 41;

QY 352 QEGFSAATISNGP--LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDS----DMNDAYLG 405
Db 181 QAGFSGIIFSDNSALVMGAPGSVYLQGIYVQSLNRSV-VQATQESNTGTVSFDNSYRG 239
QY 406 YAAAI--ILNRVQSLVLCAPYQHI-GLVAFRQNTGHWESNANVKGTQICAYFGASLC 462
Db 240 YSLALGDFNGDGVDQYVVGTPRAESLMGLVAIFDQNLQFN---QVMGTQIVAYFGYSVT 296
QY 463 SYVDVDSNGSTDVLVLCAPHYETGRGQVSVCPLRGQRARWQCDVLYGEO----- 514
Db 297 VVDI--NNDYDILLVGAPEYMDGPAIQ-----RWEAGAVYYVLQNPDPVGPQA 343
QY 515 -----GQPMGRFGAALTVLGVNGDKLTDVAIGAPCEEDNRGAVYLFHGTSGS 562
Db 344 SNRLSLSSTLIGGQIRSRFGLSIASIGDSNGDQFNDAIGAPEGDDAGAVIYHG-SAN 402
QY 563 GLSPSHSQRIAGSKLS-PRLOVFGQSLSCGQDLTMDGLVDLTGVAQ--GHVLLRSQPV 619
Db 403 GLKSTPAQVLTSTLGHSGITTFGFSLOGQDMKXKYPDILLVGAESANTAVLIRTPV 462
QY 620 RVKATMEFNPREVARNVFECNQVVKGEAGEVRVCLHVQKSTRDRFLREGQIQSV----- 674
Db 463 SLDATLNTPE-----IGINDENKTYE--LADGTWVTSFIAMT 497

Search completed: January 13, 2005, 15:13:21
Job time : 44.3983 secs

675 -----VYDLALDSG-RPHSRVAFNETKSTRQTVLGL-TQTCETLKLQ 718
Db 498 CFTYGTNYLPDHDIDISYTVTVDSGIIANRRAMFVNDMSEITKRLRAVSTQCDPLRAY 557
QY 719 LPNCIEDPVSPIVLNFSLVCTPLSAFCN-----LRPVLAEDAQRLETALPFPPEK 769
Db 558 VGNSTIEDKLTPKTKVTLQYDL-----NNDSESRLOPHEILFIIDMATWSTQTKQVSION 609
QY 770 NCGNDNIQODDLSITFSFMSLDCLVVGPGPREFNVTVVRNDCGDSYRTQVTFPFDLDSY 829
Db 610 NCVN-NICIPDLDTVT-PNLFNIVIGTQELTLDVSLNRRGEDAFQSSLSVYVPLGLQF 667
QY 830 RKVSTLQNRORSRWRLACESASSTEVSGALKSTSCSINHPIPPEN-----SEVTNIT 893
Db 668 VRL-----ERKANMDSFTCSDS-----LRIITCDTGNPMVGKNILEFGLTSLTFQVS 717
QY 884 EDVDS-----KASLGNKLLKANVTSENNMPRTNKTETQLELPVKYAVVMVTSHGVS 938
Db 718 GKDSIEFYFKAESNS--EDPNTLENNELNMTVPVTVDCUCLKLSASYEIVMWTQED 775
QY 939 YL-----NFTASENTSRVMQHOYQV-----SNLQORSLPIS-----LVFLVPV 976
Db 776 YVVPFPKAKNASEADIGMEVM-HLYEVRNTGSSNAGEVSLNIQWPKNEDGEVLFYLLGI 834
QY 977 RLNQTVIWRDPQ-----VTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1021
Db 835 MTEGVTQLTQGANPEGVKLEPSTKAKLSNSTTQVSGRKRREPEVAALAQTDN--VI 892
QY 1022 NCSIAVCORIQCDDIPFGIOEENAT-----LKGNSLFDWIKTSHNHLIVSTAEILP 1075
Db 893 YCASDSCVLINCTI-----DEINASKSKVVRILGRF--W-----ERTF 928
QY 1076 NDSVFTLLPGQAFVRSQETKEV--PFEVNP-----LP----- 1108
Db 929 QKAVSELTPVQVQATASSASAANKTIPYNIPLPRDPSDSTKASTLVTTSELPVPTPIAW 988
QY 1109 -LIVGSSVGGILLALITAALYKLGFFK-----QYKDMMS--EGGPP 1148
Db 989 WIIWVSVLGGIILLIILGLWKCGFFBRKPKGEEKEVAPVASADKGGP 1038

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 241.379 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-A
Perfect score: 5953
Sequence: 1 MALRVLTLTALTLCHGFNLD.....FKRQYKDMMSGGPPGAEPPQ 1153

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	5937.5	99.7	1152	1	ITAM_HUMAN	P1215	homo sapien
2	4542	76.3	1153	1	ITAM_MOUSE	P05555	mus musculus
3	4456	74.9	1151	2	Q9J130	Q9J130	rattus norv
4	3826.5	64.3	920	2	Q28984	Q28984	sus scrofa
5	3510	59.0	1163	1	ITAX_HUMAN	P20702	homo sapien
6	3452	58.0	1162	1	ITAD_HUMAN	Q13349	homo sapien
7	3358.5	56.4	1188	2	Q6KAS4	Q6KAS4	mus musculus
8	3358.5	56.4	1188	2	BAD21383	BAD21383	mus musculus
9	3349.5	55.1	1169	1	ITAX_MOUSE	Q9QXH4	mus musculus
10	3279.5	55.1	1161	1	ITAD_RAT	Q9QYH7	rattus norv
11	1583	26.6	1165	1	ITAL_BOVIN	P61625	bos taurus
12	1560	26.2	1170	1	ITAL_HUMAN	P20701	homo sapien
13	1557	26.2	1166	2	Q6TIB8	Q6TIB8	bos taurus
14	1557	26.2	1166	2	AAQ90015	AAQ90015	bos taurus
15	1546	26.0	1163	1	ITAX_MOUSE	P24063	mus musculus
16	1542	25.9	1161	2	Q9WTV4	Q9WTV4	mus musculus
17	1531.5	25.7	1160	2	Q9R200	Q9R200	mus musculus
18	1416	23.8	1196	2	Q9R200	Q9R200	mus musculus
19	1365.5	22.9	1187	2	Q9RTF1	Q9RTF1	cyprinus ca
20	1358	22.8	1086	2	Q9RTF0	Q9RTF0	cyprinus ca
21	1274	21.4	927	2	Q8H2V0	Q8H2V0	homo sapien
22	1168.5	19.6	1167	2	O88340	O88340	bos taurus
23	1162.5	19.5	1167	2	ITAE_MOUSE	O60677	rattus norv
24	1160	19.5	1179	1	ITAE_HUMAN	P38570	homo sapien
25	1122.5	18.9	1167	2	O88341	O88341	homo sapien
26	1105.5	18.6	1151	1	ITAI_HUMAN	P56199	homo sapien
27	1099.5	18.5	1189	1	ITAH_HUMAN	Q9UKX5	homo sapien
28	1096	18.4	1170	1	ITAX_BOVIN	P53710	bos taurus
29	1089.5	18.3	1178	2	O6PIC7	O6PIC7	mus musculus
30	1089.5	18.3	1178	2	AH65139	AH65139	mus musculus
31	1086	18.2	1178	1	ITAX_MOUSE	Q62469	mus musculus

32	1084.5	18.2	1181	1	ITAX_HUMAN	P17301	homo sapien
33	1082.5	18.2	1167	1	ITAG_HUMAN	O75578	homo sapien
34	1079	18.1	1180	1	ITAI_RAT	P18614	rattus norv
35	1065.5	17.9	1171	2	O42094	O42094	gallus gall
36	1057.5	17.8	1188	1	ITAH_MOUSE	P61622	mus musculus
37	1057.5	17.8	1188	2	O7QC3	O7QC3	mus musculus
38	1046	17.6	1038	2	Q8BS01	Q8BS01	mus musculus
39	1017	17.1	895	2	Q9WUF8	Q9WUF8	mus sp. itg
40	1014.5	17.0	1160	2	Q8MKF4	Q8MKF4	felis silve
41	865	14.5	348	2	Q8TES5	Q8TES5	homo sapien
42	849	14.3	1332	2	Q9BPQ8	Q9BPQ8	halocynthia
43	810.5	13.6	304	2	O6PG66	O6PG66	mus musculus
44	810.5	13.6	304	2	AH57200	AH57200	mus muscu
45	775	13.0	205	2	Q63001	Q63001	rattus norv

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI)
DE (Neutrophil adherence receptor).
GN Name:ITGAM; Synonyms:CR3A, CD11B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaut M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257315; PubMed=2454931;
RA Arnaut M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Paul H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=89098893; PubMed=2563162;
RA Hackett D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

Proc. Natl. Acad. Sci. U.S.A. 86:257-261 (1989).
[6]
SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaut M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and
RT developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529 (1991).
[7]
SEQUENCE OF 1-9 FROM N.A.
TISSUE=Blood;
MEDLINE=92144986; PubMed=1346576;
RA Paul H.L., Rosmarin A.G., Tenen D.G.;
RT "Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870 (1992).
[8]
SEQUENCE OF 17-31.
MEDLINE=87076671; PubMed=3339202;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
RT across species and homology to platelet IIB/IIIA.";
Biochim. Biophys. Acta 874:368-371 (1986).
[9]
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Rieu P., Arnaut M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
RT CR3 (CD11b/CD18).";
Cell 80:631-638 (1995).
[10]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RT activation";
Structure 3:1333-1340 (1995).
[11]
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE=98362595; PubMed=9687375;
RA Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
RA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,
RA Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
RA Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
RT assessment.";
Structure 6:923-935 (1998).
[12]
3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunit and a calcium binding site on its lower surface.";
Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).
CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
CC adhesive interactions of monocytes, macrophages and granulocytes
CC as well as in mediating the uptake of complement-coated particles.
CC It is identical with CR-3, the receptor for the iC3b fragment of
CC the third complement component. It probably recognizes the R-G-D
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
CC fibrinogen, factor X and ICAM1. It recognizes F1 and P2 peptides
CC of fibrinogen gamma chain.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".

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EMBL; J03925; AA59544.1; -
EMBL; M18044; AA59491.1; -
EMBL; J04145; AA59903.1; -
EMBL; S52227; AAB24821.1; -
EMBL; S52152; AAB24821.1; JOINED.
EMBL; S52153; AAB24821.1; JOINED.
EMBL; S52154; AAB24821.1; JOINED.
EMBL; S52155; AAB24821.1; JOINED.
EMBL; S52157; AAB24821.1; JOINED.
EMBL; S52159; AAB24821.1; JOINED.
EMBL; S52161; AAB24821.1; JOINED.
EMBL; S52164; AAB24821.1; JOINED.
EMBL; S52165; AAB24821.1; JOINED.
EMBL; S52167; AAB24821.1; JOINED.
EMBL; S52169; AAB24821.1; JOINED.
EMBL; S52170; AAB24821.1; JOINED.
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EMBL; S52180; AAB24821.1; JOINED.
EMBL; S52181; AAB24821.1; JOINED.
EMBL; S52184; AAB24821.1; JOINED.
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EMBL; S52191; AAB24821.1; JOINED.
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EMBL; S52212; AAB24821.1; JOINED.
EMBL; S52213; AAB24821.1; JOINED.
EMBL; S52216; AAB24821.1; JOINED.
EMBL; S52219; AAB24821.1; JOINED.
EMBL; S52220; AAB24821.1; JOINED.
EMBL; S52221; AAB24821.1; JOINED.
EMBL; S52222; AAB24821.1; JOINED.
EMBL; S52226; AAB24821.1; JOINED.
EMBL; M76724; AA58410.1; -
EMBL; M84477; AA51960.1; -
PIR; A31108; RWHUIB.
PDB; 1A8X; Model; @=17-1152.
PDB; 1BHQ; X-ray; 1/2=-.
PDB; 1IDN; X-ray; 1/2=-.
PDB; 1IDO; X-ray; @=140-331.
PDB; 1JLM; X-ray; @=143-334.
PDB; 1MU; X-ray; A=137-331.
PDB; 1NF7; X-ray; A=144-337.
PDB; 1N9Z; X-ray; A=140-335.
PDB; 1NAS; X-ray; A=144-345.
Genew; HGNC:6149; ITGAM.
MIM; 120980; -
GO; GO:0008305; C: integrin complex; TAS.
GO; GO:0007155; P: cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00092; VWA; 1.
Pfam; PF001185; INTEGRIN.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0234; VVFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
Transmembrane.

RX MEDLINE=86287312; PubMed=2942940;
 RA Sastre L., Roman J.M., Teplov D.B., Dreyer W.J., Gee C.E.,
 RA Larson R.S., Roberts T.M., Springer T.A.;
 RT "A partial genomic DNA clone for the alpha subunit of the mouse
 RL Complement receptor type 3 and cellular adhesion molecule Mac-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
 [4]
 RN SEQUENCE OF 17-28.
 RP MEDLINE=85188276; PubMed=3887182;
 RA Springer T.A., Teplov D.B., Dreyer W.J.;
 RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
 RL glycoproteins and unexpected relation to leukocyte interferon.";
 RL Nature 314:540-542(1985).
 CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
 CC adhesive interactions of monocytes, macrophages and granulocytes
 CC as well as in mediating the uptake of complement-coated particles.
 CC It is identical with CR-3, the receptor for the iC3b fragment of
 CC the third complement component. It probably recognizes the R-G-D
 CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
 CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
 CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
 CC mast cell development and in immune complex-mediated
 CC glomerulonephritis. Mice expressing a null mutation of the alpha-M
 CC subunit gene demonstrate increase in neutrophil accumulation, in
 CC response to a impaired degranulation and phagocytosis, events that
 CC apparently accelerate apoptosis in neutrophils. These mice develop
 CC obesity.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P05555-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P05555-2; Sequence=VSP_010473;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X07640; CAA30479.1; -;
 DR EMBL; AK039444; BAC30350.1; -;
 DR EMBL; M14293; AAA39484.1; -;
 DR FIP; S00551; S00551.
 DR HSSP; P11215; 1BHQ.
 DR MGD; MG1:96607; Itgam.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0007155; P:cell adhesion; IMP.
 DR GO; GO:0045123; P:cellular extravasation; IMP.
 DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWFA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

DR PROSITE; PS00234; VWFA; 1.
 KW Alternative splicing; Calcium; Cell adhesion;
 KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 1153 Integrin alpha-M.
 FT DOMAIN 17 1105 Extracellular (Potential).
 FT TRANSMEM 1106 1129 Potential.
 FT DOMAIN 1130 1153 Cytoplasmic (Potential).
 FT REPEAT 31 84 FG-GAP 1.
 FT REPEAT 85 163 FG-GAP 2.
 FT DOMAIN 164 350 VWFA.
 FT REPEAT 337 400 FG-GAP 3.
 FT REPEAT 401 452 FG-GAP 4.
 FT REPEAT 454 515 FG-GAP 5.
 FT REPEAT 517 575 FG-GAP 6.
 FT REPEAT 580 632 FG-GAP 7.
 FT CA_BIND 465 473 Potential.
 FT CA_BIND 529 537 Potential.
 FT CA_BIND 592 600 Potential.
 FT SITE 1132 1136 GPPKR motif.
 FT DISULFID 66 73 By similarity.
 FT DISULFID 105 123 By similarity.
 FT DISULFID 654 711 By similarity.
 FT DISULFID 770 776 By similarity.
 FT DISULFID 999 1023 By similarity.
 FT DISULFID 1028 1033 By similarity.
 FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 772 772 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 801 801 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 881 881 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 941 941 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 980 980 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 994 994 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1022 1022 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1051 1051 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1076 1076 N-linked (GlcNAc...) (Potential).
 FT VARSPATIC 453 569 Missing (in isoform 2).
 FT FTID=VSP_010473.
 FT CONFLICT 37 37 N -> S (in Ref. 2).
 FT CONFLICT 683 683 V -> G (in Ref. 2).
 SQ SEQUENCE 1153 AA; 127480 MW; 178DB988AECB0343 CRC64;
 Query Match 76.3%; Score 4542; DB 1; Length 1153;
 Best Local Similarity 74.4%; Pred. No. 3.9e-290;
 Matches 859; Conservative 142; Mismatches 151; Indels 2; Gaps 2;
 QY 1 MALRVLLLTALTLCGHNLDTENAMTQBNARGQSVVQLGSRVVVGAPQEIIVANQR 60
 DB 1 MTLKALLVTALALCHGFGNLDTEHPMTQENAKGFQNVVLGGTSVVVAAPQEKAVNQ 60
 QY 61 GSLYQCDYSTGSCPIRLQVPEAVNMNLSGLSLAATSPPOLLAGCTVHTCSENTVVK 120
 DB 61 GALLYQCDYSTGSCPIPLQVPEAVNMNLSGLSLAATSPPOLLAGCTVHTCSENTVVK 120
 QY 121 GLCFLFGSNLRQPKQKPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMBQL 180
 DB 121 GLCYLFGSNLLRPQKPEALRGCPQEDSDIVFLIDGSGSINNTDFQKMKFVSTVMBQF 180
 QY 181 KSKSTLFLSMQYSEFRIHFTFKFQNNPNRSLVKPITQLLGHHTATGTRKVVRELFN 240
 DB 181 KSKSTLFLSMQYSEFRIHFTFKFQNNPNRSLVKPITQLLGHHTATGTRKVVRELFN 240
 QY 241 ITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVDAPRSKSRQEL 300
 DB 241 ITNGARENAKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVDAPRSKSRQEL 300

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QY 301 NTIASKPRDRHVQVNNFEALKTIONQREKXFAIEGTQTGSSSFEHMSQEGFSAAIT 360
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 301 DTIASKPAGEHFVQVDFNEALNTIQLOQEKIFAIEGTQTGSSSFEHMSQEGFSASIT 360
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDTVA 540
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDTVA 540
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 541 ICAPGEENRGAVLYPHGTSGSGISPSHSORITAGSKLSPLOYFGOSLGGGDLTMDGLV 600
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 540 ICAPGEENRGAVLYPHGTSGSGISPSHSORITAGSKLSPLOYFGOSLGGGDLTMDGLM 599
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 601 DLTGVAQGHVLLLRQSVPLRVKAIIMEFNPREVARNVFECNDQVVRKGEAGEVRVCLHVQK 660
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 600 DLAVGAQGHVLLLRQSVPLRVKAIIMEFNPREVARNVFECNDQVVRKGEAGEVRVCLHVQK 659
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 661 STRDLRREGIQSVVTVYDIALDSGRPHSRVAVNETKNSRTRQVGLTQTCETLKLQLP 720
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 660 NTKDLRREGIQSVVTVYDIALDSGRPHSRVAVNETKNSRTRQVGLTQTCETLKLQLP 719
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 721 NCIEDPVPIVLRNPLSVLGTPLSAGNLRPLVLAEDAQRLFTALPFEKNCNDNICODD 780
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 720 DCVDSVSPILRLNLTLLGEPFLRSGNLRPLVLAEDAQRLFTALPFEKNCNDNICODD 779
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 781 LSITPSFMSLDCLVGGPREFNVTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNGRS 840
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 780 LSITPSFMSLDCLVGGPREFNVTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNGRS 839
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 841 QRSWRL-ACESASSTEVSGALKSTCSINHPFPENSEVTFNITPDVDSKASLGKLLIK 899
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 840 KKPWFVKPAESSSSSEGHGALKSTTNINHPFPANSEVTFNITPDVDSKASLGKLLIK 899
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 900 ANVTSENMPRTNKTETFOLELVKAVVNVTVSHGVSTKYNLFTASENTRVMQHOYQVS 959
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 900 ALVASENNMSRTHKTKFQLELVKAVVNVTVSHGVSTKYNLFTASENTRVMQHOYQVS 959
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 960 NLGQSLPISLVLPVRLNQTVIWDPRQVTFSENLSSCTCHTKERLPSHSDFLAELRKAP 1019
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 960 NLGQSLPISLVLPVRLNQTVIWDPRQVTFSENLSSCTCHTKERLPSHSDFLAELRKAP 1019
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1020 VVNCISVACQRIQCDIPFFGIQEEFNATLKNLSFDWYIKTSHNHLIVSTAEILFNDSV 1079
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1020 VVNCISVACQRIQCDIPFFGIQEEFNATLKNLSFDWYIKTSHNHLIVSTAEILFNDSV 1079
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1080 FTLLPQGFVFSOTETKVEPEVNPLPLIVGSSVGLLALITAAALYKLGPFKROVK 1139
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1080 FALLPQGESYVRKSTETKVEPEVNPLPLIVGSSVGLLALITAAALYKLGPFKROVK 1139
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1140 DMWSEGGPPGABPQ 1153
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1140 DMWSEGGPPGABPQ 1153
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 3
Q9J130
ID Q9J130 PRELIMINARY; PRT; 1151 AA.
AC Q9J130;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Integrin beta 2 alpha subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
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[1]
SEQUENCE FROM N.A.
Fathallah D.M. Sr., Zerrila K. Jr.;
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-1- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
HSP; P11215; 1BHQ.
GO; GO:0008305; C:protein complex; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; WFAADOMAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS00234; VWA; 1.
Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;
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Query Match 74.9%; Score 4456; DB 2; Length 1151;
Best Local Similarity 73.4%; Pred. No. 1.8e-284;
Matches 846; Conservative 145; Mismatches 160; Indels 2; Gaps 2;

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QY 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGSVVQLOGSVVVCAPQEIIVAAQOR 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 MTLKLLVLTALTLCHGFNLDTENAMTFQENARGFQGSVVQLOGSVVVCAPQEIIVAAQOR 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GSLYQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATTPPQALLAGCTVHQCSENTYVK 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GALYQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATTPPQALLAGCTVHQCSENTYVK 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 GLCFPLGSLNLRQKQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQL 180
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 GLCYFLGSLNLRQKQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQL 180
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 KSKTFLSLMOYSEFRTHFTFKFQNNPNRSLVKPITOLLGRTHATGIRKVVRELEN 240
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 QKSKTFLSLMOYSEFRTHFTFKFQNNPNRSLVKPITOLLGRTHATGIRKVVRELEN 240
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 241 TNGARKNAKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVGFADFRSEKROEL 300
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 241 KINGARDNAKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVGFADFRSEKROEL 300
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 301 NTIASKPRDRHVQVNNFEALKTIONQREKXFAIEGTQTGSSSFEHMSQEGFSAAIT 360
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 301 DTIASKPAGEHFVQVDFNEALNTIQLOQEKIFAIEGTQTGSSSFEHMSQEGFSAAIT 360
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
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QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDTVA 540
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDTVA 540
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 541 ICAPGEENRGAVLYPHGTSGSGISPSHSORITAGSKLSPLOYFGOSLGGGDLTMDGLV 600
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 540 ICAPGEENRGAVLYPHGTSGSGISPSHSORITAGSKLSPLOYFGOSLGGGDLTMDGLM 599
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 601 DLTGVAQGHVLLLRQSVPLRVKAIIMEFNPREVARNVFECNDQVVRKGEAGEVRVCLHVQK 660
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 600 DLAVGAQGHVLLLRQSVPLRVKAIIMEFNPREVARNVFECNDQVVRKGEAGEVRVCLHVQK 659
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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DT 01-FEB-1991 (Rel. 17, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
 DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Ileu M5).
 GN Name=ITGAX; Synonyms=CD11c;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=8816645; PubMed=3327687;
 RX Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
 RA "cDNA cloning and complete primary structure of the alpha subunit of a
 RT leukocyte adhesion glycoprotein, p150,95.";
 RL EMBO J. 6:4023-4028(1987).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90153906; PubMed=2303426;
 RX Corbi A.L., Garcia-Aguilar J., Springer T.A.;
 RA "Genomic structure of an integrin alpha subunit, the leukocyte p150,95
 RT molecule.";
 RL J. Biol. Chem. 265:2782-2788(1990).
 RN [3]
 RN ERRATUM.
 RP Corbi A.L., Garcia-Aguilar J., Springer T.A.;
 RL J. Biol. Chem. 265:12750-12751(1990).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan J., Moore I., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., Loewell N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 20-43.
 RP MEDLINE=87167596; PubMed=3549901;
 RX Miller L.J., Wiebe M., Springer T.A.;
 RA "Purification and alpha subunit N-terminal sequences of human Mac-1
 RT and p150,95 leukocyte adhesion proteins.";
 RL J. Immunol. 138:2381-2383(1987).
 CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
 CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
 CC interaction during inflammatory responses. It is especially
 CC important in monocyte adhesion and chemotaxis.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.

-!- DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11c.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M81695; AA59180.1; -;
 DR EMBL; M29165; -; NOT ANNOTATED CDS.
 DR EMBL; M29487; AA51620.1; ALT SEQ.
 DR EMBL; M29482; AA51620.1; JOINED.
 DR EMBL; M29483; AA51620.1; JOINED.
 DR EMBL; M29484; AA51620.1; JOINED.
 DR EMBL; M29485; AA51620.1; JOINED.
 DR EMBL; M29486; AA51620.1; JOINED.
 DR EMBL; BC038237; AAH38237.1; -;
 DR PIR; A36584; RWHU1C.
 DR PDB; 1N3Y; X-ray; A=141-338.
 DR Genew; HGNC:6152; ITGAX.
 DR MIM; 151510; -;
 DR GO; GO:0008305; C:integrin complex; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0009887; P:organogenesis; TAS.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; WFAADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS0234; VWFA; 1.
 DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
 KW Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 1163 Integrin alpha-X.
 FT DOMAIN 20 1107 Extracellular (Potential).
 FT TRANSMEM 1108 1128 Potential.
 FT DOMAIN 1129 1163 Cytoplasmic (Potential).
 FT REPEAT 34 87 FG-GAP 1.
 FT REPEAT 88 ? FG-GAP 2.
 FT DOMAIN 165 351 VWFA.
 FT REPEAT 401 401 FG-GAP 3.
 FT REPEAT 402 453 FG-GAP 4.
 FT REPEAT 455 517 FG-GAP 5.
 FT REPEAT 518 576 FG-GAP 6.
 FT REPEAT 581 633 FG-GAP 7.
 FT CA_BIND 466 474 Potential.
 FT CA_BIND 530 538 Potential.
 FT CA_BIND 593 601 Potential.
 FT SITE 1131 1135 GPFKR motif.
 FT DISULFID 69 76 By similarity.
 FT DISULFID 108 126 By similarity.
 FT DISULFID 655 712 By similarity.
 FT DISULFID 771 777 By similarity.
 FT DISULFID 848 863 By similarity.
 FT DISULFID 998 1022 By similarity.
 FT DISULFID 1027 1032 By similarity.
 FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 392 392 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 697 697 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 939 939 N-linked (GlcNAc...) (Potential).

FT	CARBOHYD	1050	1050	N-linked (GlcNAc...) (Potential).
FT	VARIANT	48	48	W -> R (in dbSNP:11574633).
FT				/FTId=var_018672.
FT	CONFLICT	209	209	T -> S (in Ref. 4).
FT	CONFLICT	251	251	T -> A (in Ref. 4).
FT	CONFLICT	469	469	T -> S (in Ref. 4).
FT	CONFLICT	490	490	G -> A (in Ref. 2).
FT	CONFLICT	547	547	E -> K (in Ref. 4).
FT	CONFLICT	756	756	D -> L (in Ref. 4).
FT	CONFLICT	819	819	I -> V (in Ref. 4).
FT	CONFLICT	1163	1163	SEK -> tPHYQDNV (in Ref. 4).
FT	TURN	150	157	
FT	TURN	160	161	
FT	HELIX	164	178	
FT	TURN	179	180	
FT	TURN	183	185	
FT	TURN	186	193	
FT	STRAND	197	201	
FT	HELIX	203	208	
FT	HELIX	212	216	
FT	TURN	217	218	
FT	STRAND	226	226	
FT	HELIX	228	236	
FT	TURN	237	240	
FT	HELIX	242	244	
FT	TURN	245	245	
FT	TURN	248	249	
FT	STRAND	251	258	
FT	STRAND	263	263	
FT	HELIX	269	278	
FT	TURN	279	280	
FT	STRAND	282	288	
FT	HELIX	290	293	
FT	TURN	296	297	
FT	HELIX	298	304	
FT	HELIX	310	312	
FT	STRAND	313	316	
FT	HELIX	319	325	
FT	HELIX	326	334	
FT	TURN	335	335	
SQ	SEQUENCE	1163 AA;	127886 MW;	83658A13B5C5DE8F CRC64;
Query Match				
Best Local Similarity 59.0%; Score 3510; DB 1; Length 1163;				
Matches 700; Conservative 139; Mismatches 296; Indels 6; Gaps 4;				
QY	5	VLLLTALTLCHGNLDTENAMTFQENARGFGQSVVQLQGRVYVVCAPQEIIVAAANQSGSLY	64	
DB	8	LLLTALATSLGFLNLTBELTAFRVDSAGFGDSVVQYANSWWVVGAPQKITAANQTGGLY	67	
QY	65	QCDYSTGSCPIRLQVPVEAVNMISLGLSLAATSPPLQALLACGPTVHQTCSNTYVKGLCF	124	
DB	68	QCQYSTGACEPIGLQVPEAVNMISLGLSLASTTSPSLLACGPTVHCEGGRNWTGLCF	127	
QY	125	LFGSNLRQOPKQFPEALRGCPQEDSDIAPLIDGSGSIIPHDPFRMKFVSTVMEQLKSK	184	
DB	128	LLGPT--QLTQRLPVSRQECPRQEQDIFVLIDGSGSISSRNFAWMNFVRAVISQFORPS	185	
QY	185	TLFSLMOWSEEPRIHTPEKQNNPRSLVKPITQLGRHTATGIRKVRLENING	244	
DB	186	TOFLMQSNKPFQTHTEEFEEFARTSNPLSLASVHQLQGTYYTATAIQNVVHRLFHASYG	245	
QY	245	ARKNAFKILVITDGEKFDPLGYEDVTPADREGVIRYVIGVDAPRSEKSRQSLNTIA	304	
DB	246	ARRDATKILVITDGEKGDSDLYKDVIPMADAAGIIRYAGVGLAFQNRNSWELNDIA	305	
QY	305	SKPPRDHVPQNNFALKTIQNLREKXPAIEGTGTGSSSFSEHMSQEGFSAATISNGP	364	
DB	306	SKPSQEHIFKVEDFDALXDIQNLKEKIFAIEGTETTSSSFSELEMAQEGFSAVFTPDGP	365	
QY	365	LLSTVGSVDWAGGVFLYTSKEKSTFINTRVDSQNDMAYLGVAAAILRNVSQSLVLCAP	424	
DB	366	VLGAVGSFTWSGGAFLYPPNMSPTFINMSQENVDNRDYSYLGYSTELALWKGVQSLVLGAP	425	

QY	425	RYOHIGLVAMPRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVE	484	
DB	426	RYOHTGKAVITQVSRQRMKAQVGTQIGSTFGASLCSVDVDTGSTDVLVIGAPHYVE	485	
QY	485	QTRGGQSVSVCLPRGORARWQCDVLYGEOQOPWGRFGAALTVLGDVNGDKLTDVAIGAP	544	
DB	486	QTRGGQSVSVCLPRGWR--RWCDAVLYGEOQWGRFGAALTVLGDVNGDKLTDVVGAP	544	
QY	545	GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLAPRLOYFGQSLSGGGQDLTWGDLVDLTV	604	
DB	545	GEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSRLOYFGQALSGGGQDLTQDGLVDLAV	604	
QY	605	GAQGHVLLRSOPVLRVKAIIMEENPREVAFECNDQVVKGEAGEVRVCLHVOKSTRD	664	
DB	605	GARGVLLLRTPVLWVGVSQGFPAEIPRFAFECREQVSEQTUVQSNICLIYIDKRSKN	664	
QY	665	RLREGQIQSVVYTDIALDSGRPHSAFVNETKNSRRQTQVLGTLTQTCETIKLQLPNCIE	724	
DB	665	LLGSRDLQSSVTLDLADPGRLSPRATFQETKNRSLSRVRLGLKAHCENFLLLPSCVE	724	
QY	725	DPVSPVLRLNPSLVGTPLSAFGNLRPVLAEDAQRLFTALPFPKNCNNDNICODDLISIT	784	
DB	725	DSVTPTILRLNFTLVGKPLAFRLNLRPLMAADAQRYFTASLPFEKNCGADHICQDNLGIS	784	
QY	785	FSPMSLDCLVVGGPREFNVTVRNDGSDSYRTQVTRFFPLDLSYRKVSTLQNRQSRSM	844	
DB	785	FSPGLKSLVNGSNLELNAEVMVWNGDSDSYRTITFHPAGLSYRYVABQKQQLRSL	844	
QY	845	RLACESASTREVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANVTS	904	
DB	845	HLTCDSAPVG--SQGTWSTSCRINHLIFRGCAQITFLATFDVSPKAVLGDRLLTANVSS	902	
QY	905	ENMPTNKTEFOLELPVKYAVVMVTSHGVSYKYLAFITAS-ENTSRVMQHOYQVSNLQ	963	
DB	903	ENMPTSKTTFQLELPVKYAVYTVWSSHEQFTKYLNFSESESEKESHVAMERYQVNNLQ	962	
QY	964	RSLPISLVFLVRLNQTIVWDRPQVTFPNSLSTCTCHTERLPSSHDSFLAELRKPVVNC	1023	
DB	963	RDLPVSNFVWVPELVNQAEMVWDEVSHQPNSLRCSSEKIAPASDFLAHIQKNPVLDC	1022	
QY	1024	SIACVQRIQCDIPFFGIQEFNATLKNLSFDWYKTSNHNLLIVSTABILLPNDVSFTLL	1083	
DB	1023	SIAGCLPRCDVPVSFQSELDFTLKGNSLSEGWRLQKKVSVVSVVAIEITFDTSVYSQL	1082	
QY	1084	PGQAFVRSOTETKVEPEVPEVNPPLIVGSSVGGLLLALITALYKLGFKPKQYKQWMS	1143	
DB	1083	PGQAFVRAQTTTLEKYKVNHPPLIVGSSIGGLLLALITAVLYKVGFPRQYKEMME	1142	
QY	1144	E 1144		
DB	1143	E 1143		
RESULT 6				
ITAD_HUMAN				
ID	ITAD_HUMAN	STANDARD;	PRT;	1162 AA.
AC	Q13349; Q15575; Q15576;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).			
GN	Name=ITGAD;			
OS	Homo sapiens (Human);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=961111956; PubMed=8777714;			
RA	Van der Vliet H., Le Trong H., Wood C.L., Moore P.F., St John T.,			
RA	Stanton D.E., Gallatin W.M.;			

RT "A novel leukointegrin, alpha d beta 2, binds preferentially to IGAM-
 RL 3.";
 RL Immunity 3:683-690(1995).
 RN [2]
 RP SEQUENCE OF 1-235 FROM N.A.
 RA MEDLINE=20187620; PubMed=10722744;
 RX Noti J.D., Johnson A.K., Dillon J.D.;
 RT "Structural and functional characterization of the leukocyte integrin
 RL gene Cldd. Essential role of Sp1 and Sp3.";
 RL J. Biol. Chem. 275:8959-8969(2000).
 RN [3]
 RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
 RX MEDLINE=96257236; PubMed=8666289;
 RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
 RT "Cloning and chromosomal localization of a novel gene-encoding a human
 RL beta 2-integrin alpha subunit.";
 RL Gene 171:291-294(1996).
 RN [4]
 RP INTERACTION WITH VCAM1.
 RX MEDLINE=99059842; PubMed=9841932;
 RA Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
 RX Hoffman P.A., Staunton D.E., Bochner B.S.;
 RT "alpha2beta2 integrin is expressed on human eosinophils and functions
 RL as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
 RL 1).";
 RL J. Exp. Med. 188:2187-2191(1998).
 RN [5]
 RP INTERACTION WITH VCAM1.
 RX MEDLINE=99370002; PubMed=10438935;
 RA Van der Vieren M., Crowe D.T., Hoekstra D., Vazquez R., Hoffman P.A.,
 RX Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
 RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
 RL binding interface between I domain and VCAM-1.";
 RL J. Immunol. 163:1984-1990(1999).
 CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
 CC clearing lipoproteins from plaques and in phagocytosis of blood-
 CC borne pathogens, particulate matter, and senescent erythrocytes
 CC from the blood.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
 CC associates with beta-2.
 CC -!- SURCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
 CC lines and subsets of peripheral blood leukocytes and strongly on
 CC tissue-specified cells, including macrophages foam cells within
 CC atherosclerotic plaques, and on splenic red pulp macrophages.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC -----
 DR EMBL; U37028; AAB38547.1; -;
 DR EMBL; U40274; AAB60634.1; -;
 DR EMBL; U40275; AAB60635.1; -;
 DR EMBL; U40276; AAB60636.1; -;
 DR EMBL; U40277; AAB60637.1; -;
 DR EMBL; U40279; AAB60638.1; -;
 DR EMBL; U40278; AAB60638.1; JOINED.
 DR EMBL; AF187881; AAF62875.1; -;
 DR HSSP; P11215; 1BHQ.
 DR Genew; HGNC:6146; ITGAD.
 DR MIM; 602453; -;
 DR GO; GO:0008305; C:integrin complex; TAS.
 DR GO; GO:0016337; P:cell-cell adhesion; NAS.

DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWFA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS02334; VWFA; 1.
 DR Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 1162 Integrin alpha-D.
 FT DOMAIN 18 1100 Extracellular (Potential).
 FT TRANSMEM 1101 1121 Potential.
 FT DOMAIN 1122 1162 Cytoplasmic (Potential).
 FT REPEAT 32 85 FG-GAP 1.
 FT REPEAT 86 ? FG-GAP 2.
 FT DOMAIN 150 332 VWFA.
 FT REPEAT 350 400 FG-GAP 3.
 FT REPEAT 401 452 FG-GAP 4.
 FT REPEAT 454 516 FG-GAP 5.
 FT REPEAT 518 576 FG-GAP 6.
 FT REPEAT 581 633 FG-GAP 7.
 FT CA_BIND 465 473 Potential.
 FT CA_BIND 530 538 Potential.
 FT CA_BIND 593 601 Potential.
 FT SITE 1127 1131 GFFKR motif.
 FT DISULFID 67 74 By similarity.
 FT DISULFID 106 124 By similarity.
 FT DISULFID 655 710 By similarity.
 FT DISULFID 769 775 By similarity.
 FT DISULFID 846 861 By similarity.
 FT DISULFID 994 1018 By similarity.
 FT DISULFID 1023 1028 By similarity.
 FT CARBOHYD 59 59 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 87 87 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 99 99 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 691 691 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 733 733 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 873 873 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 957 957 N-linked (GlcNAc..?) (Potential).
 FT CARBOHYD 1046 1046 N-linked (GlcNAc..?) (Potential).
 FT CONFLICT 500 500 Missing (in Ref. 2).
 FT CONFLICT 515 518 GHPW -> ATP (in Ref. 2).
 FT CONFLICT 825 825 L -> V (in Ref. 2).
 FT CONFLICT 984 984 V -> A (in Ref. 2).
 SQ SEQUENCE 1162 AA; 126885 MW; F296A1A35455D77D CRC64;
 Query Match 58.0%; Score 3452; DB 1; Length 1162;
 Best Local Similarity 59.9%; Pred. No. 2.9e-218;
 Matches 683; Conservative 163; Mismatches 287; Indels 8; Gaps 6;
 QY 5 VLLLTALTLCHGNLDNTENAMTFQENARGFGQSVVVLQGSRRVVGAPQEIIVAAVNRGSLY 64
 DB 6 VLLLSVLASYHGNLDVBEPTIPOEDAGGQSVVVGFGSRRVVGAPLEVVAAVNRGSLY 65
 QY 65 QCDYSTGSCPTIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVKGSLC 124
 DB 66 DCAATGNCQPIPLHIREAVNMSLGLSLAATNGSRLACGPTLHRCVGENSYSGSL 125
 QY 125 LFGSNLRQOPKFPALRGCPQEDSDIAFLIDGSGIIPHFRMKFVSTVWEQKKSK 184
 DB 126 LLGSRW-EIIQTVPDATPECPHQEMDIVFLIDGSGIDQNDPNQMKGFVQAVMGQFEGD 184
 QY 185 TLFSLMYSSEFRHTFTKEQNPNPSLVKPTQLGLGRHTATGIRKVVRELFINING 244
 DB 185 TLFALMYSNLLKHTFTFTQRTSPSQSLVDPIVQLKGLTFTATGILTFTVVTQLPHRNG 244

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QY 245 ARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIA 304
DB 245 ARKSAKKILVITDGQKYDPLEYSDVIPAQEKAGIIRYVIGVGHAFQPTARQELNTIS 304
QY 305 SKPPRDHVPQVNNFALKTIQNLREKPAIBGTGTGSSSSPEHEMSQEGFSAATSNRP 364
DB 305 SAPPQDHVFKVDFNFAALGSIQLOEKIYAVGTQSRASSSPQHEMSQEGFSTALTMDEL 364
QY 365 LLSTVGSYDWMAGVFLYTSKEKSTFINTRVDSMDNDAYLGAALILRNVRQSVLIGAP 424
DB 365 FUGAVGSFSWGGATFLPPNMPSTFINMSQENVDNRDYLGVSTELALWKGVQNLVLGAP 424
QY 425 RYQHIGLVAMFRQNTGMWESNANVKTQIGAYFGASLCSVDVDSNGSDTLVLIGAPHYYE 484
DB 425 RYQHTGKAVITQVSRQWRKKAETVGTQIGSYFGASLCSVDVDSNGSDTLVLIGAPHYYE 484
QY 485 QTRGGQVSVCPPLPRGORARWQCDVLYGEGQPGWRFGAALTVLGVNNGDKLTVVAIGAP 544
DB 485 QTRGGQVSVCPPLPRGORVQWQCDVLRGEGQHPWGRFGAALTVLGDVNEKDLIDVAIGAP 544
QY 545 GEEDNRGAVYLPFGTSGSGISPSHSQRTAGSKLSPLOYFGQSLGGODLTMDELGLVDTV 604
DB 545 GEQENRGAVYLPFGHASEGISPSHSQRTASSQLSPRLQYFGQALSGGQDLTQDGLMDLAV 604
QY 605 GAQGHVLLRSQPLVLRVKAIMEFNPREVARNVFECDQVVGKEAGEVRVCLVHVKSTRD 664
DB 605 GARGQVLLRLSLPVLKGVWRFSPVEVAKAYRQWEEKPSALEAGDATVCLTIQKSSLD 664
QY 665 RUREGOISVTVYDIALDSGRPHSRVAVNETKSTRQTVLGLPQTCETKLQLPNCIE 724
DB 665 QL--GDIQSSVRFDLALDPGRULTSRAIFNETKNPTLTRKTLGLGHCETKLKLLPDCVE 722
QY 725 DPVSPVLRLNPLSVCTPLSARGNLRPVLAEDAPRLFTALPFEKNCNGNDNICQDLSIT 784
DB 723 DVVSPILILHNLFSLVREPIPSQNLRLPVLAGSQDLFTASLPFEKNCQDGLCEGDLGVT 782
QY 785 FSFMSLDCLVGGPREFNVTVTRVDGDSYRQVTFPPFLDLSYRKVSTLQNRQSRW 844
DB 783 LSFSGQLTLTVGSSLELVNIVTVWAGDSYGTVVSLLYYPAGLSHRVSGAQPHQSAL 842
QY 845 RIACSSASTSVSGALKSTSCSINHPIIPENSEVTNITFDVDSKASLGNKLLKANVTS 904
DB 843 RLACETV--PTEDEG--LRSSRCSVNHPIFHEGNGTFTVTFDVSYKATLGDRLMFASS 900
QY 905 ENNMPTNKTEFQLELPVKYAVVMVTSHGVSCTKYNF--TASENTRVMQHOYQVSNLQ 963
DB 901 ENNKASSKATFQLELPVKYAVITMISQEBSTKYFNATSDKKQKAEHRVYNNLSQ 960
QY 964 RSLPLSLVFLVRLNQTVINDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVC 1023
DB 961 RDLAISINFWPVLNGVAVWDMVMEAPSQSL--PCVSEKPPQHSDFLTQISRSPMLDC 1018
QY 1024 STAVCORIOCDIPFGIEEFNATLKNLSFDWYIKTSHNHLIVSTAEILFNDSVFTLL 1083
DB 1019 STADCLQCRDVPFSVQEBELDTLKNLSFGWVRETLLQKVLVVSVAEITFDTVSQSL 1078
QY 1084 PCOGAFVSOTETKVEPEVNPPLPIYGVSSVGGILLALITAAALKLGFKKQYKDMMS 1143
DB 1079 PQQAFMRQAEQMWLEEDVEYNAIPIIMGSSVGALLLALITATLYKLGFKKRYKEMLE 1138
QY 1144 E 1144
DB 1139 D 1139
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RESULT 7

Q6KAS4

ID Q6KAS4

AC Q6KAS4

DT 05-JUL-2004

DT 05-JUL-2004

DT 05-JUL-2004

DT 05-JUL-2004

PRELIMINARY; PRT; 1188 AA.

(Tremblrel. 27, Created)

(Tremblrel. 27, Last sequence update)

(Tremblrel. 27, Last annotation update)

```
DE MFLJ00114 protein (Fragment).
GN Name=mFLJ00114;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AK131133; BAD31383.1; -.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA_1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS50234; VWFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON TER 1
SQ SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;

Query Match 56.4%; Score 3358.5; DB 2; Length 1188;
Best Local Similarity 57.2%; Pred. No. 4.4e-212;
Matches 658; Conservative 167; Mismatches 307; Indels 19; Gaps 7;

QY 6 LLLTALTLCFGLNDTENAMTFQGNARGFGQSVVQLQSGRVVVGAPQSIIVANORGSLYQ 65
DB 28 LLLGFGVSLGFLNDAEKPTFHMDGAEFGHSVLYQYDSSVWVGAPREIKATNQIGLYK 87
QY 66 CDYSTGSCPEIRLQVPVEAVNMSLGLSLAATSPQLLACGPTVHQTSCENTYVKGCLFL 125
DB 88 CGYHTGNCPEISLPVPEAVNMSLGLSLAATNPSSLACGPTVHHTCRENIIYLTGLCFL 147
QY 126 FGSNLRQOPQFPALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKT 185
DB 148 LSSSFQKS-QNFPYTAQCEPKQDQDIVFLIDGSGSISSTDPEKMLDFYKAVMSQLQRPST 206
QY 186 LFSLMQYSEBPIRHPTKPEFONNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGA 245
DB 207 RFSLMQSDYPRVHFTNFNFISTSPSLDLSVQLRGYTTTASAKHVIITELFTQSGA 266
QY 246 RKNATKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIAS 305
DB 267 RQDATKVLIVITDGRKQGNLSYDVPMAEASIIRYAIGVKAFYNEHKSQELKATAS 326
QY 306 KPPRDHVPQVNNFALKTIQNLREKPAIBGTGTGSSSSPEHEMSQEGFSAATSNQPL 365
DB 327 MFSHEYVFSVNFDAKDIENQLKEKIPAIETGTTSPSSSTFELEMSQEGFSAVTPDGPV 386
QY 366 LSTVGSYDWMAGVFLYTSKEKSTFINTRVDSMDNDAYLGAALILRNVRQSVLIGAPR 425
DB 387 LGAVGSFSWGGATFLYPSNMRPTFINMSQENEDNRDAYLGYSTALAFWKGVHSLILGAPR 446
QY 426 YQHIGLVAMFRQNTGMWESNANVKTQIGAYFGASLCSVDVDSNGSDTLVLIGAPHYYEQ 485
DB 447 HQHTGKVVITQESRHRWRPKSEVGTQIGSYFGASLCSVDMDRDSGSDTLVLIGVPHYYEH 506
QY 486 TRGGQVSVCPPLPRGORARWQCDVLYGEGQPGWRFGAALTVLGVNNGDKLTVVAIGAP 545
DB 507 TRGGQVSVCPMP-GVGRRWCHCGTTLHGEQGHQHPWRFGAALTVLGVNNGDSDLADVAIGAP 565
```


Db 1041 HMOKSPVLDSCDCLHLRCDIPSGILDELYFIKGNLSFGWISQTLQKKVLLSEAEI 1100
 QY 1074 LPNDSVFTLLPQGAQVRSQTEKVEPVPNPLPLIVGSSVGGGLLALLALITAAALYKLG 1133
 Db 1101 TENTSVPQLPQGAFLRAQTKVLEMYKVNPNPLIVGSSVGGGLLALLAITAILYKAGF 1160
 QY 1134 FKQYKDMME 1144
 Db 1161 FKQYKEMLEE 1171

RESULT 9
 ITAX MOUSE
 ID ITAX MOUSE STANDARD; PRT; 1169 AA.
 AC Q9QXH4;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
 DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
 GN Name=Igax;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dendritic cell;
 RA Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
 RA Tsuchiya H.;
 RT "Isolation of genes selectively expressed by dendritic cells.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
 CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
 CC interaction during inflammatory responses. It is especially
 CC important in monocyte adhesion and chemotaxis (By similarity).
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
 CC associates with beta-2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF211864; AAF23492.1; -.
 DR HSSP; P20702; IN3Y.
 DR MGD; MG1:96609; IGax.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR020335; VWFA.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00092; Integrin_alpha; 1.
 DR Pfam; PF00092; VWFA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS00234; VWFA; 1.
 KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1169 Integrin alpha-X.
 FT DOMAIN 20 1116 Extracellular (Potential).

FT TRANSMEM 1117 1137 Potential.
 FT DOMAIN 1138 1169 Cytoplasmic (Potential).
 FT REPEAT 34 87 FG-GAP 1.
 FT REPEAT 88 2 FG-GAP 2.
 FT DOMAIN 152 330 VWFA.
 FT REPEAT 403 454 FG-GAP 3.
 FT REPEAT 456 518 FG-GAP 4.
 FT REPEAT 519 577 FG-GAP 5.
 FT REPEAT 582 634 FG-GAP 6.
 FT REPEAT 667 745 FG-GAP 7.
 FT CA_BIND 467 475 Potential.
 FT CA_BIND 531 539 Potential.
 FT CA_BIND 594 602 Potential.
 FT SITE 1140 1144 GFFKR motif.
 FT DISULFID 69 76 By similarity.
 FT DISULFID 108 126 By similarity.
 FT DISULFID 656 711 By similarity.
 FT DISULFID 770 776 By similarity.
 FT DISULFID 858 873 By similarity.
 FT DISULFID 1007 1031 By similarity.
 FT DISULFID 1036 1041 By similarity.
 FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 949 949 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1059 1059 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1084 1084 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;
 Query Match 56.3%; Score 3349.5; DB 1; Length 1169;
 Best Local Similarity 57.0%; Pred. No. 1.7e-211;
 Matches 656; Conservative 169; Mismatches 307; Indels 19; Gaps 7;
 QY 6 LLLTALTLCFNLDTENAMTFQENARGCGSVVQLQGSRRVVGAPQIIVANQSGSLYQ 65
 DB 9 LLLGLFVSLGFLNDAEKLTHFHMGAFHGHVLYQDSSWVVGAPKEIKATNQIGGLYK 68
 QY 66 CDYSTGSCPTRLQVPVEAVNMVLSLAATSPPLLACGPTVHQTCESTYVKGCLFL 125
 DB 69 GYHTGCEPISLQVPPPAVNIISLSLAATNSWLLACGPTVHHTCRENIIYLTGLCFL 128
 QY 126 FGSNLRQOPKQFPALRCPOEDSDIAPLIDGSGSIIPHDPFRMKBFVSTVMEQLKSKT 185
 DB 129 LSSSFQKS-QNFTAAQPCQDQDIVFLIDGSGSISSTDFEKLDFKAVMSQLRPS 187
 QY 186 LPSLMQYSEERIHFTKFEQNNPNPSLVPIQLLGRTHATCIRKVVLELNITNGA 245
 DB 188 RPSLMQFSYDPRVHFTFNNFISTSPULSLGSRQLRGYTYTSAIKHVIITELFTTQSGA 247
 QY 246 RKNAPKILVITDGEKFDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIAS 305
 DB 248 RQDATKVLIVTDGKQGNLSYDSVIPMAEASTIYRVAIGVKAFYNEHSKQELKATAS 307
 QY 306 KPPRDHVFQNNFALKTIQNLREKXPAIGTGTGSSSEHEMSQSGFAATSNPL 365
 DB 308 MPSEHYVFSVENFDALKDIENQLKEKIPAEIGETTPSSSTFELEMSQSGFSAVTPDGPV 367
 QY 366 LSTVGSYDMAGVLYTSKESKSTFNMTNRVSDMNDVLYGAAAILLRNRRVQSLVIGAPR 425
 DB 368 LGAVGSFWSGGAFLYPSNMRPTFINMSQENEDMRDYLGYSTALAFWKVGHSLILGAPR 427
 QY 426 YQHIGLVAMFRONTGMWESNANVKTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYEEQ 485
 DB 428 HQTGKVIVFTQESHWRPKSEVRGTQIGSYFGASLCSVDMDRDSSTDLVLIGVPHYEH 487
 QY 486 TRGGQSVCLPRQRARWQCDVLYGQGGQFWRFGAALTIVLGDVNGDKLTDVAIGAPG 545
 DB 488 TRGGQSVCPMP-GVGSRWHCCTTLHGRQHPWRFGAALTIVLGDVNGDSLADVAIGAPG 546
 QY 546 EEDNRGAVLYFHTGSGCISPSHSQRIAGSKSLRPOLYFGOSLGGQDLTMDGLVDLTVG 605
 DB 547 BEENRGAVIIFHGASRQDIAPSPQSQRISASQIPRIQIFGOSLGGQDLTMDGLVDLTVG 606

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QY 606 AGHVLLRSQVLRVKAIMEFNPBVARVNEPCNDVVVKGEAEVVRVCLHVQKSTRDR 665
D 607 SKGRVLLRLTRILRVSPVTHFPAEISRSVEQEQVAPEQTLSDATVCLHIESPKTQ 666
QY 666 LREGIOISVVYDLDALDGRPHSRVAFNETKNSRRQVQLGLTQCTCLKQLPNCLED 725
D 667 L--GDLRSVTVFDLADHGRLSRAIFKTRKTRALTRVKTGLNKHCSVKULLPACVED 724
QY 726 PVSPIVLNFSLVGTPLSAFANLRPLVAEDAQRLFTALFPPEKNCNDNICQDLSITF 785
D 725 SVTPITLRLNFSLVGVPISSLQNLQPLAVDDQTYFTASLPEKNCADHICQDLSVVF 784
QY 786 SPMSDCLVGVGRFNVTVVRNDEGSYRTQVTFPPPLDLSYKXVSTLQ----- 836
D 785 GFPDLKTLVVGSDLELVNVDVTVSNDGDSYGTVTFLFVPGVLSFRRAEGQVFLRKEDQ 844
QY 837 --NORSQSRWLACESASTEVSGALKSTSCSINPIPIPENSEVTFNITEDVDSKASLGN 894
D 845 QWRQGRQSHLWMD--STPDRSQGLMSTSCSRHIVFRGSGQMTFLVTFVSPKAELED 902
QY 895 KLLKANTYSENMPRTNKRTERQLELPVKYAVYVMVTVSHGVSTKYLNFTASE--NTRVYMQ 953
D 903 RLLLRARVGSNNVPTKTTQLELPVKYAVYTMISSHDQTKYLNFTSEKETSVE 962
QY 954 HOYQVSNLQGRSLPISLVFLVPLRNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLA 1013
D 963 HRFQVNNLQGRDVPVSVINFWBIELKGEAV--TVMVSHVQNPQLTCYRNRLKPTQFDLLT 1021
QY 1014 ELRKAPVNCSTAVCORLOCDIPFGIOEEFNATLGNLSFDWYIKTSHNLLIYVSTAEI 1073
D 1022 HMQKSPVDCSTADCLHURCDIPSGILDELFIKGNLSFGWISQTLQKKVLLSEAEI 1081
QY 1074 LFNDSVFTLLPQCAFVSQRTKVEPFPVNPPLIVGSSVGGGLLALLIATAALYKLG 1133
D 1082 TPTSVYSGLPQEAFLRAQTKVLEMYKVNPLIVGSSVGGGLLALLIATAALYKAGF 1141
QY 1134 FRQYKQWMSSE 1144
D 1142 FRQYKEMLEE 1152

RESULT 10
ITAD RAT
AC ITAD RAT STANDARD; PRT; 1161 AA.
ID Q9QE7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA O'Brien M.M., Vandervieren M., Kilgannon P.D., Dietsch G.,
RA Gallatin W.M.;
RT "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: belongs to the integrin alpha chain family.
```

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CC CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC CC -!- SIMILARITY: Contains 1 VWFA domain.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AF021334; AAF21241.1; --
CC CC HSSP; P11215; 1BHQ.
CC CC InterPro; IPR000413; Integrin_alpha.
CC CC InterPro; IPR002035; VWF_A.
CC CC Pfam; PF01839; FG-GAP; 3.
CC CC Pfam; PF00357; Integrin_alpha; 1.
CC CC Pfam; PF00092; VWF; 1.
CC CC PRINTS; PR01185; INTEGRINA.
CC CC PRINTS; PR00453; VWFADOMAIN.
CC CC SMART; SM00327; VWF; 1.
CC CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC CC PROSITE; PS50234; VWFA; 1.
CC CC Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
CC CC Repeat; Signal; Transmembrane.
CC CC SIGNAL 1 19 Potential.
CC CC CHAIN 20 1161 Integrin alpha-D.
CC CC DOMAIN 20 1100 Extracellular (Potential).
CC CC TRANSMEM 1101 1121 Potential.
CC CC DOMAIN 1122 1161 Cytoplasmic (Potential).
CC CC REPEAT 34 87 FG-GAP 1.
CC CC REPEAT 88 ? FG-GAP 2.
CC CC REPEAT 152 334 VWFA.
CC CC REPEAT 352 402 FG-GAP 3.
CC CC REPEAT 403 454 FG-GAP 4.
CC CC REPEAT 456 517 FG-GAP 5.
CC CC REPEAT 519 577 FG-GAP 6.
CC CC REPEAT 582 634 FG-GAP 7.
CC CC CA_BIND 531 539 Potential.
CC CC CA_BIND 594 602 Potential.
CC CC SITE 1126 1130 GFFKR motif.
CC CC DISULFID 69 76 By similarity.
CC CC DISULFID 108 126 By similarity.
CC CC DISULFID 656 711 By similarity.
CC CC DISULFID 769 775 By similarity.
CC CC DISULFID 845 860 By similarity.
CC CC DISULFID 993 1017 By similarity.
CC CC DISULFID 1022 1027 By similarity.
CC CC CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 784 784 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 936 936 N-linked (GlcNAc...) (Potential).
CC CC CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).
CC CC SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;
CC CC -----
CC CC Query Match 55.1%; Score 3279.5; DB 1; Length 1161;
CC CC Best Local Similarity 58.0%; Pred. No. 6.8e-207;
CC CC Matches 662; Conservative 159; Mismatches 306; Indels 15; Gaps 10;
CC CC -----
QY 5 VLLLT--ALTCHGNLDTENAMTPQENARFGQSVVQLQGSRVVVGAPQETVAANQRGS 62
D 6 VLLCGWVLSCHGSLNLDVEPIVREDAAISFGQVTVQVFGGSRVVGAPLEAVAVNQTR 65
QY 63 LYQCDYSYSGCEPIRLQVPEAVNMSLGLSAAATTSPPQLLACGPTVHTQCSSENTYVKGL 122
D 66 LYDCAPATGMCPQIVILRSPLEAVNMSLGLSVTATNNAQLLACGPTAQRACVKNMYAKGS 125
```


FT	DISULFID	842	858	By similarity.	
FT	DISULFID	994	1009	By similarity.	
FT	DISULFID	1017	1048	By similarity.	
FT	CARBOHYD	33	33	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	86	86	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	185	185	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	646	646	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	667	667	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	723	723	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	859	859	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	894	894	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	929	929	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	1056	1056	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	1067	1067	N-linked (GlcNAc. .)	(Potential).
SQ	SEQUENCE	1165	AA; 128725 MW; DAEBA3AF1E1463CB CRC64;		
Query Match					26.6%; Score 1583; DB 1; Length 1165;
Best Local Similarity					34.8%; Pred. No. 4.8e-95;
Matches 417; Conservative 200; Mismatches 475; Indels 108; Gaps 34;					
QY	1	MALRVLLLTALTL--CHGFNLDTENAMTFQENARG--FGQSVVQLQGSRVVVGAPQEIIVA	56		
DB	6	IVLRLLSGPFVPAPAWSNLDVRHVQNFSPPLAGRHFGYRVLQV--GNGVVVGAPSE---61			
QY	57	ANQRGLYQCDYSTGCEPIRLQVPEAVNMSIGLSLAATTPPQALLACGPTVHQTCSEN	116		
DB	62	GNSMGNLYQCPETGDCLPVTL--SNYTSKYLGMTLATDPTSDNLLACDPLGSLRTCDQN	119		
QY	117	TVYKGLCFPLGSNLRQOPKFFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKKEVSTV	176		
DB	120	IYLSGLCYLIHENLRGVVQGHGQYCEIKGNVDLVLPDFDGSMSLQODEFKIVDFPMKDV	179		
QY	177	MEQLKSKTFLSLMOYSEBFRIHFTKFBQNNPNRSLVKPTQLLGRTHRTATGRKVVVR	236		
DB	180	MXKLSNSYQFAAVQSFYTFTEFLDIYRKQDPDALLAGVKHMLLNTTCAINYVAK	239		
QY	237	ELFNITNGARKNAKILVITGEKFGPLGVEDVIPEADRGVIRVYIVGVGDAPRSEKS	296		
DB	240	EVFRPLDGLARPATKVLIIITDGEATD----EHNIDAA--KDIIRYIIIGIKGNFKTKES	292		
QY	297	RQELNTIASKPRDHVQVNNFEALTIQNLREKXFALEGQTQSGSSSPEHEMSQEGES	356		
DB	293	Q8ALHOFASKPVEEFVKIIDLTFEKLKDLFTLQKLIYIEGTSKQDLTSFNELSSSGIS	352		
QY	357	AAITSGNPLSTVSGDAGGVF--LYTSKEKSTFINMTRVDSMDNDAYLGYAAA--ILLRN	414		
DB	353	ADLSEGHVGVGAGKADWAGGLDLKADLKSTFFVGNELPTVESRAGLYGYVWLPSPRG	412		
QY	415	RVQSLVLGAPRYOHIGLVAMFRQ--NTGMWESNANVKGTOIGAYFASLCSVDVDSNGST	472		
DB	413	TMSLLATGAPRYQHVGRVLLFQPKRGPGPWSQIETDGIQIGSYFGGELCGVDVDRDGET	472		
QY	473	DLVLIGAPHYEOTRGQGVSVCLPLRGQARWQCDALVYGEQOPKRGFGAALTVLGDVN	532		
DB	473	ELLIIIAPIYGGQGRGVFY---QKIQLEPQWSELQOETGYPRFGAALAAALTDIN	529		
QY	533	GBKLTDAIACPEEDNRGAVLFIHSTGSGISPSHSQRIAGSLPRILQYFQSLSGQ	592		
DB	530	GDELTDAVAGAPLEE--QGANVIFNQOG--GLSPRESQRIEQTQMSGQWFGRSIHGVK	586		
QY	593	DLTMDGLVLTVGAQGHVLLRSQPLRVKAIMFNPREVARNVFNCNDQVVKGEAG--E	651		
DB	587	DLGGDGLADVAGAEQVIVLSRPVVDIITSVSFPABIPVEHEVCYSTSNQKKEGVN	646		
QY	652	VRVCLHVQK--STRDLRLEGQISVVTYDLALDSGRPHSRAPVNEFNSTRQTVLGLT	709		
DB	647	LTVCFQVKKSLIST-----FQGHVLANIYTLQLDGHRTSRGLFPFGKHLIGNVATVPV-	701		
QY	710	QTCETLKLQLPNCIEDPVPSPVLRINFSL---VGTPLS--AFGNLRLPVLAEQAQRLFTAL	764		
DB	702	KSCFVFWFHPICIQDLISPINVLSYSLWEEGTFRDPRALDRDIPPIKLPSPHLETKE	761		
QY	765	FPEKNCNDNICQDLSITFSFMSLDCLVWGGPREFNVTVTVRNDGEDSYRTQVTFPPF	824		

RESULT 12

ITAL_HUMAN

ID	ITAL_HUMAN	STANDARD;	PRT; 1170 AA.
AC	P20701; O43746;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	01-OCT-2004 (Rel. 45, Last annotation update)		
DE	Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1		
DE	alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha		
DE	chain) (CD11a).		
GN	Name=ITGAL; Synonyms=CD11a;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.		
RX	MEDLINE=89139587; PubMed=2537322;		
RA	Larson R.S., Corbi A.L., Berman L., Springer T.;		
RT	"Primary structure of the leukocyte function-associated molecule-1		
RT	alpha subunit: an integrin with an embedded domain defining a protein		
RT	superfamily.";		
RL	J. Cell Biol. 108:703-712(1989).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RX	MEDLINE=99425270; PubMed=10493829;		
RA	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,		
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,		
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,		
RA	Bichler E.B., Harris P.C., Venter J.C., Adams M.D.;		
RT	"Genome duplications and other features in 12 Mb of DNA sequence from		
RT	human chromosome 16p and 16q.";		
RL	Genomics 60:295-308(1999).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214.		
RX	MEDLINE=96036067; PubMed=7479767;		
RA	Qu A., Leahy D.J.;		
RT	"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha L		
RT	beta 2) integrin.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995).		
RN	[4]		
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 153-335.		
RX	MEDLINE=96398682; PubMed=8805579;		
RA	Qu A., Leahy D.J.;		
RT	"The role of the divalent cation in the structure of the I domain from		

Matches	409;	Conservative	211;	Mismatches	464;	Indels	110;	Gaps	38;
Qy	6	LLLTALTLCHGF	-----	NLDTENAMTFQ	--ENARGEQSQSVYVQLQSGRRVVVGAPQEI	54			
Db	6	ITVAMALLSGFFFPFAPASSYNLNDRGARGSFSPPRAGRHFGYRLQV	-----	NGVIVGAPGE	-63				
Qy	55	VAANQRSLLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPVPHOTCS	114						
Db	64	--GNSTGSLYQCOSGTGCHLPVTLR	-GSNTYSKYLGMTLATDPTDGGILACDPLGSRCTD	120					
Qy	115	ENTVVGKLCFLFGSNLR	---QQPQKEPEALRGCPQEDSDIAFLIDGSGSTIIPHDFRMM	170					
Db	121	QNTVLSGLCYLFRNLQCPMLQGRPGQECIKG	---NVDLVFLFDGSMLSLQDFEFOKI	176					
Qy	171	EFVSTVMEQLKSKTFLSMQYSBEFRIHFTFKFQNNPNRSLVAKTITOLLGRTHRTATG	230						
Db	177	DFMKDVMMKLSNTSYQFAAQVQFSYKTEPDFSDYVVRKDPDALLKHVKHMLLTNTFGA	236						
Qy	231	IRKVVRELFINTGARKNAKFLIIVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA	290						
Db	237	INTVATVVFRELGARPDATKVLIIITDGE	-ATDSGNIDAADK-----IIRVIIGTCKH	289					
Qy	291	FRSEKSRQELNTASKPRDHVFOVNNFEALKTIQNOLREKKAFAIEGTQCTSSSPHEHM	350						
Db	290	PQTKESQETLHKFASKPASBFVKILDTPEKLUFTLQKKIYVIEGTSKODLTSFNEL	349						
Qy	351	SOEGFSAIITSNGPLLTSTVGSYDWAGGVF	-LYTTSKEKSTFINNTRVDSNMNDAYLVGAAA	409					
Db	350	SSSGISADLSRGHAVGAVGAKWAGGFLDLKADLQDTPFIGNEPFLPEVRAGVLGYTVT	409						
Qy	410	-IILNRNVQSLVLGAPRYOHIGLVAMFR	-QNTGMWESNANVKGTQITQVGFAGSLCSVDV	466					
Db	410	WLPSRQKTSLLASGAPRYQHMGRVLLFQEPQGGHWSQVQTIHQTCIGSYFGGELCGVDV	469						
Qy	467	DSNGSTDVLIGAPHYYEQTREGGQSVCPPLPRGARWQCDAY	--LYGEOGQPWGRGAA	524					
Db	470	QDQGETELLIGAPLFYGEORGGRVFIY	---QRQLGFEFVSELOQDGPYPLGRFGEA	524					
Qy	525	LTVLGDVNGDKLTDVAITGAPGEEDNRGAVYLFHGTSGSIGSPSHSORIAGSKLSPRQYF	584						
Db	525	ITALTDINGDGLVDVAGAPLEE	-QGANVIFNGRHG-GLSPQSPQRIEQTQVLVSLGLOWP	581					
Qy	585	QOSLSGGQDUTMDGLVDLTVAAGHVLILLRSQPVLRVKAIMEFNPREVARNVFECNQVV	644						
Db	582	GRSITHGVKLEGDLADVAVGAESQMIIVLSRPVDMVTLMSFPABIPVHEVBCSSTS	641						
Qy	645	-KGKEAGEVRVCLHVQKSTRDLREGQIQSVVTYDLDALDGRPHSRVAFNETKNSTRQT	703						
Db	642	NMKKEGYNITICFOI	-KSLYPQF-QGRGLVANLYTYLQLDGHRTRRGLFGGRHGLARNI	699					
Qy	704	QVLGLTQTCETLKLQLPNCIEDPVSPTVLRNFSL	---VGTPLS--AFGN-----LRPVL	753					
Db	700	AVT-TSMSCITDPSFHPVVCQDLISPLNVSINLSLWEEBGTPRDQRAQGDIPPLRPSL	758						
Qy	754	AEDAQRLLFTALPPKKNCGNDNICQDLSLSTFSFMSLDCLVVGGRFBNVTVTRNDGED	813						
Db	759	HSETWEI	---PEKKNCGEDKKCEANLRVSPSPARSRALRLTAFASLSVELSLSNLEED	813					
Qy	814	SYRTQVTFPPDLDSYRKVSTLQNRQSRWRLACES	--ASSTEVSGALKSTSCSINHPI	871					
Db	814	AYWQLDLHFPFGLSFRKVEML	---KPHSQIPVSCSELPEESRLLSRAL---SCNVSSPI	867					
Qy	872	FPENSEVTFINITPDVDKASLGNKLLKANVTSSNN	---MPRTNKTEFQLELPPKVAVY	927					
Db	868	FKAGHSVALQMMFNTLVNSWGDSVELHANVTCTNEDSDLLLEDNSATTI	---IPILYPIN	924					
Qy	928	MVVTSHGVSTKYLNTFASNTSRVMQHQYQV	---SNLQGRSLP-ISLVFLVPRVLNQTVI	983					
Db	925	ILIQDQEDSTLYVSTFKPGKPIHQVKMYQVRIQPSIHDHNIPTLEAVVGVPQPPSGEPI	984						
Qy	984	WDRPQVTFSENLSSTCHTK	--ERLPSHD--FLAELRKAPVNVGSIACVQRIQCIDIFFG	1039					
Db	985	THOWSQVMEPPV	--PCHYEDLERLPDAEPCPLGALPRCPW-----	1024					

Qy	1040	IQEFNATLKNGLSFDWYIKTSNHHLLIVSTAIELFNDSVFTLLPGGQAFVRSQTETKVE	1099
Db	1025	FRQIBLVQVIGTLELVGEIAS-SMFSGSLSGISFNSSHFHLYGNSAL-AQVNMKVD	1082
Qy	1100	PFEVNPPLPIVGVSSVGLLILLITAAALYKLGFFKQYKDMKSEG-GPPCAEP	1152
Db	1083	VVEKQMLXYIVLSGIGGLLLLLLIFIVLYKVGFRRNLKEMKAGRGVNGIP	1136
RESULT 13			
Q6TVB8		PRELIMINARY;	
ID	Q6TVB8	PRT;	1166 AA.
AC	Q6TVB8		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Lymphocyte function-associated antigen 1 alpha subunit CD11a.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).		
CC	-1- SIMILARITY: Belongs to the integrin alpha chain family.		
DR	EMBL; AY382558; AAQ90015.1; -		
DR	InterPro; IPR004113; Integrin_alpha.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF01839; FG-GAP; 1.		
DR	Pfam; PF00357; Integrin_alpha; 1.		
DR	Pfam; PF00092; VWA; 1.		
DR	PRINTS; PR01185; INTEGRINA.		
DR	PRINTS; PR00453; VWFADOMAIN.		
DR	SMART; SM00191; Int_alpha; 5.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.		
DR	PROSITE; PS00234; VWFA; 1.		
DR	Cell adhesion; Integrin; Transmembrane.		
KW	Cell adhesion; Integrin; Transmembrane.		
QY	SEQUENCE	1166 AA; 128723 MW; 7B8D8AFBA896C9DF CRC64;	
Query Match 26.2%; Score 1557; DB 2; Length 1166;			
Best Local Similarity 34.2%; Pred. No. 2.5e-93;			
Matches 411; Conservative 203; Mismatches 478; Indels 108; Gaps 34;			
Qy	1	MALRVLLLTALT--CHGFNLDTENAMTFQENARG--FGOSVVLQSGSRVVVGAPQIIVA	56
Db	7	IVRLLLSGFVFAPAWSYNLDRVHVNQFSEPLAGRHFGVRVLQV-GNGVVVGAPSE---	62
Qy	57	ANORGSILYCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATTPQLIACGPTVHQTCSEN	116
Db	63	GNSMGNLVQCPETGDCPLVTL--SNYTSKYLGTLTATDPTSDNLACDPLGSLRTCDQN	120
Qy	117	TVYKGLCFGLSGNLRQOPQFPFALRCCPOEDSDIAFLIDGSGSIIPHDFRMKEFVSTV	176
Db	121	IYLSGLCYLTHENLRGPVLQGHFGYQCIKGNVDLVELFDGMSLQODEFEKIVDFMKDV	180
Qy	177	MEOLKKSKTFLSLMOYSEERPIHFTKFQNNPNRSLVKRPIQLLGRTHTATGIRKVR	236
Db	181	MKLSNSSYQFAAVQFSTYFTEFFLDYIKQKDPDALLAGVKHMLLTWTFGAINYVAK	240
Qy	237	ELFNITNGARKAFKILVWITDGEKFGDPLGYEDVITPEADREGVIRVVIQVGDAPRSEK	296
Db	241	EVERPDIGARPDATKVLIIITDGK--PPTNTTILMRPKTSS---RSLLGIGKNFKTKES	293
Qy	297	ROELNTIASKPRDHPVQVNNFEALKTIQNLREKFAISGTOTGSSSSFEHEMSQGF	356
Db	294	QEAHQFASKPSEVFVKILDTFFEKLDLFTLEQKIVIEGTQKDIYSFNMELSSSGIS	353
Qy	357	AAITNSGPIILSTVGSYDWAGGVF-LYTSKEKSTFFINMTRVDSMDNDAYLVGAAA-IILRN	414

Db 354 ADLSEGHGVGAVGAKWAGGFLDLKADLKSSTFGVNEPLTVESRAGLYGTVTRLPKRG 413
Qy 415 RVQSLVILGAPRYOHTGLVAMFRQ--NTGMWESANVKGTOIGAYGASLCSVDVDSNGST 472
Db 414 TMSLLATGAPKYQHVGRVLLFPQKRGFPWSQIQBIDGIGQISYFGGLCGVDVDRDGET 473
Qy 473 DLVLICAPHYEQTGGGVSVCPPLRGORARQCDAVLYGEOGPWGRFGAALTIVLGDVN 532
Db 474 ELLILTAAPLYGEOGRGVFIY--QKLEFQWVSELOGETGYPLGRFGAIAALTIDIN 530
Qy 533 GDKLTDVAIGAPGEDNRGAVLPHGTSGSISPSHSQRIAGSKLSPRLQVFGQSLSGGQ 592
Db 531 GDELTDVAVGAPLEE--QGVAVIFNGQOG--GLSPRPSQRIEGTQMFSGIOWFGRSIHGK 587
Qy 593 DLTMDGLVDLTVGAQGHVLLRSQPLRVKAIMFNPREVARNVFECDQVVKGEAG-E 651
Db 588 DLGGDLADVAVGAGGVIVLSSRPVDDIITSVSFSPAEPVHEVECSYSTSNQKKEGVN 647
Qy 652 VRVCLHVQK--STRDLREGQIQSVVTVDLALDSGRPHSRVAFNETKSTRQTQVLGIT 709
Db 648 LTVCFQVKSLLIST-----FQGHVLANLTYTLQDGHRTSRGLFPGGKHKLIGNTAVTPV- 702
Qy 710 QTCETLKLQPCNIEDPVPSPIVLRLNFSL---VGTPLS--AFGNLRPVLAEADAQLFTAL 764
Db 703 KSCFVFWFHPFICIQDLISPINVLSYSLWESEGTFRDPRALDRDIPPIKPSPHLETKE 762
Qy 765 PFPEKNCNDNICQDDLSITFSFMSLDCLVGGPREFNVTVVRNDGEDSTRTQVTFPP 824
Db 763 IPFEKNCEDKNCEADKLAFSDMRSKILRLTPSASLVRLTRNTAEDAYVQVTLSPFP 822
Qy 825 LDLSYKRVSTLQNRQSQRSLACESASSTVSGALKSTSCSINHPIPPENSEVTFNITF 884
Db 823 QGLSPRKVEILL---KPHSHVPVGCCELPEAVVHS--RALSNCVSSPIFGESWDIOWMF 878
Qy 885 DVDSKASLGNKLLKANVTS-----ENNMPRTNKTEFQLELPVKYAVVMVTVSHGVS 936
Db 879 NTLQKSGWDGFIELQANVSCNEDSLLSDNATS-----IPVMYPINVLTKDQENS 931
Qy 937 TKYLNFTASENTSRVMQHOYQV----SNLQGRSLPISLVFLVPLVRLNQTIV---WD---R 986
932 TLVIGSFTPKSPRIHVKHLYQVRIQPSNDNMP--PLEALVRVPRVHSEGLITHKWSIQME 990
987 POWTFS--ENLSTCHTKERLPKSHSDFLAELRKAPVNVCSIAVCORIQCDIPFGIQEBFN 1045
991 PFWNCSPRNLESDEAE-----SCSFGI--EFCRPIDF--RQELT 1027
1046 ATLKNLSPDWIKTSHNHLIVSTAEILFNDVSVFTLLPGQAFVRSQTETKVEBPEVFN 1105
1028 VQVNGMVELRGITIKAS--SMLSLSCLSLAISFNSSKHFLHGRNASM--AQVVMKVDLVYEKE 1085
1106 PLPLTVGSSVGGILLALLALITALYKLGFPKQYKDDM-----SEGPPGAEPQ 1153
1086 MLYVYLSGIGGILLLLFLIFIALYKVGFPKRNKMEANVDASSEIPGEDAGQPELEKE 1145

RESULT 14

AAQ90015
ID AAQ90015 PRELIMINARY; PRT; 1166 AA.
AC AAQ90015,
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Lymphocyte function-associated antigen 1 alpha subunit CD11a.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Dillepan T., Thumikak P., Kannan M.S., Maheswaran S.K.;
RT "Molecular cloning and sequencing of bovine CD11a."

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY382558; AAQ90015.1; -.
SQ SEQUENCE 1166 AA; 128723 MW; 7B8D8AFBA896C9DF CRC64;
Query Match 26.2%; Score 1557; DB 2; Length 1166;
Best Local Similarity 34.2%; Pred. No. 2.5e-93;
Matches 411; Conservative 203; Mismatches 478; Indels 108; Gaps 34;
Qy 1 MALVLLLTALT--CHGFNLDTENAMTFQENARG--FGQSVVOLQSGVVVVAQPOEIVA 56
Db 7 IVRLLLSGPPVAFAPASINLUDVRHVQVNSPPLAGRHGYVLQV--GNGVVVGAPSE--- 62
Qy 57 ANORGSLYCCDYSCSEPIRLQVPEAVNMNLSGLSLAATTPPQLLACGTVHQTCSN 116
Db 63 GNSMGNLYQCQPETGDCPLVTL--SNYTSKVLGWTLATDPTSDNLLACDPLSRTCDQ 120
Qy 117 TVYKGLCHLFGSNLRQOPQKFEALRGCPQSDIAFLIDGSGIIPHDPFRMKEFVSTV 176
Db 121 IYLSGLCYLIHENLRGPVLQGHGPGYQECIKGNVDLVFLFDGMSLQDQDEFKIVDFMKDV 180
Qy 177 MEOLKSKTFLSLMOYSEPRIFHTFEFQNNPNRSLVKPITOLLGRTHTATGIRKVV 236
Db 181 MKLNSNSYQFAAQVQFSTYFTEFTFLDYIKQDPDALLAGVKHMLLTNTFGALNYAK 240
Qy 237 ELFNITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPRSKS 296
Db 241 EVFRPDLGARPDATKVLIIITDGK---PPTNTLMRPKTSS---RSLGIGKPKTKES 293
Qy 297 ROELNTASKPRDHVFOVNNFEALKITQNLREKXFAIEGTQTCGSSSFEHMSQEGFS 356
Db 294 QEALHQFASKVEFVFKILDTFEKLKDLFTLQKIVYIEGTSKODLTSFNKLSLSSSGIS 353
Qy 357 AAITNSGPLLSTVGSYDWAGVF--LYTSKEKSTFINMTVRVSDMNDAYLGA---IILRN 414
Db 354 ADLSEGHGVGAVGAKWAGGFLDLKADLKSSTFGVNEPLTVESRAGLYGTVTRLPKRG 413
Qy 415 RVQSLVILGAPRYOHTGLVAMFRQ--NTGMWESANVKGTOIGAYGASLCSVDVDSNGST 472
Db 414 TMSLLATGAPKYQHVGRVLLFPQKRGFPWSQIQBIDGIGQISYFGGLCGVDVDRDGET 473
Qy 473 DLVLICAPHYEQTGGGVSVCPPLRGORARQCDAVLYGEOGPWGRFGAALTIVLGDVN 532
Db 474 ELLILTAAPLYGEOGRGVFIY--QKLEFQWVSELOGETGYPLGRFGAIAALTIDIN 530
Qy 533 GDKLTDVAIGAPGEDNRGAVLPHGTSGSISPSHSQRIAGSKLSPRLQVFGQSLSGGQ 592
Db 531 GDELTDVAVGAPLEE--QGVAVIFNGQOG--GLSPRPSQRIEGTQMFSGIOWFGRSIHGK 587
Qy 593 DLTMDGLVDLTVGAQGHVLLRSQPLRVKAIMFNPREVARNVFECDQVVKGEAG-E 651
Db 588 DLGGDLADVAVGAGGVIVLSSRPVDDIITSVSFSPAEPVHEVECSYSTSNQKKEGVN 647
Qy 652 VRVCLHVQK--STRDLREGQIQSVVTVDLALDSGRPHSRVAFNETKSTRQTQVLGIT 709
Db 648 LTVCFQVKSLLIST-----FQGHVLANLTYTLQDGHRTSRGLFPGGKHKLIGNTAVTPV- 702
Qy 710 QTCETLKLQPCNIEDPVPSPIVLRLNFSL---VGTPLS--AFGNLRPVLAEADAQLFTAL 764
Db 703 KSCFVFWFHPFICIQDLISPINVLSYSLWESEGTFRDPRALDRDIPPIKPSPHLETKE 762
Qy 765 PFPEKNCNDNICQDDLSITFSFMSLDCLVGGPREFNVTVVRNDGEDSTRTQVTFPP 824
Db 763 IPFEKNCEDKNCEADKLAFSDMRSKILRLTPSASLVRLTRNTAEDAYVQVTLSPFP 822
Qy 825 LDLSYKRVSTLQNRQSQRSLACESASSTVSGALKSTSCSINHPIPPENSEVTFNITF 884
Db 823 QGLSPRKVEILL---KPHSHVPVGCCELPEAVVHS--RALSNCVSSPIFGESWDIOWMF 878
Qy 885 DVDSKASLGNKLLKANVTS-----ENNMPRTNKTEFQLELPVKYAVVMVTVSHGVS 936
Db 879 NTLQKSGWDGFIELQANVSCNEDSLLSDNATS-----IPVMYPINVLTKDQENS 931
Qy 937 TKYLNFTASENTSRVMQHOYQV----SNLQGRSLPISLVFLVPLVRLNQTIV---WD---R 986

Db	176	MDVWRKLSNTSYQFAAVQFSTDCRTEFTFYDYVKQKNPNVDVLGSGVQPMELLNTPRAI	235
Qy	232	RKVVERLFIINTGARKNAFKLVITDGEKFGDPLGYEDVIFEADREG-----VIRYV	284
Db	236	NYVVAHVFKESGARPDATKVLVIITDG-----EASDKGNISAAHDITRYI	281
Qy	285	IGVGDAFRSEKSRQELNTIASKPRPDHVQVNNFEALKTIONQREKXFAIEGTQSGSS	344
Db	282	IGIKGHFVSQOKTHLFIASEPVEEFKILDTFTPEKLDLFTDQRRYIAEYENRQDLT	341
Qy	345	SFEHMSQEGFSAAITSNGPLLSTVGSVDWAGGYF-LYTSKEKSTFFINMTDVGSDMNDAY	403
Db	342	SFNWELSSGSIADLSKCHAVVGAGAKWAGGFLDREDLQGAATFVQOEPPLTSDVRGGY	401
Qy	404	LGYAAA-IILNRNVQSLVLGAPRYOHTGLVAMFR--QNTGMWESNANVKYQIGAYFGAS	460
Db	402	LGYTVAWMTSSRSRPLLAAGAPRYQHVQVQLLFOAPEAGGRWNQTKIEGTQIGSYFGGE	466
Qy	461	LCSVDVDSNGSTDVLVIGAPHYVBSQTGGGVSVCPLRGPORARQCDVAVLGEQGQWGR	520
Db	462	LCSVDLDQDGEAEULLIGAPLFGQERGRVFTY---QRRSLFEMVSELOQDDPEYFLGR	518
Qy	521	FGAALTVLVDVNGDKLTDVAIGAPEEEDNRGAVLDFHGTSGSGLSPSHSQRISAGLSLPR	580
Db	519	FGAAITALTDLINGDRLTDVAVGAPLEE--QGVAVIFNGKPG-GLSPQSPQRIQGAQVFPG	575
Qy	581	LOYEGOSLGGODLTMDGLVDLTVGAOGHVLLLRSQPVLRYKVAIWENPREVARNVEECN	640
Db	576	IRWFGRIHGKVDLGGDRDLADVGAAGRVVLLSSRPVVDVVVTLSPSPSEIPIVHEVECS	635
Qy	641	DQVVKGEAG-EVRVCLHVOKSTRDLRREGIOQSWVTYDLALDSGRPHSRAVFNETKNST	699
Db	636	YSAREEQKHGVKLKACAFRIKPLTPQ--FOGELLANLSYTLQDGHWRSRCLFPDGSHEL	693
Qy	700	RRQTQVLGLTQCTETLKLQLPNCIEDPVSPIVLRKNSLV---GTPJUSAFGN-LRPVLAE	755
Db	694	SGNTSITP-DKSCULDFHFHFCIQDLISPTNVSLNFSLLIEEGTPTDKGRAMQPTLRP	752
Qy	756	DAQRLFTALPFPEKNCNDNICODDLISITFSFMSLDCLVWGGP-----REFNVTVTVRN	809
Db	753	SIHTV-TKEIPFEKNCGEDKCEANLILSPARS-----GPIRLMSSASLAVETWLSN	804
Qy	810	DGEDSYRTQVTFPFPDLVSRKYSTLQNQRSQRWRLACSASSTEVSGAL-KSTSCSIN	868
Db	805	SGEDAYVWRLLDLPFRGLSPFAKVMELQ---PHSRMPVSCBEL--TEGSSLLITKLKCNVS	859
Qy	869	HPIPENSEVTFNLTDFVDKASLGNKLLKANVTSEN-NWPRNTKTEFQLELPLVKVAVY	927
Db	860	SPIFKAQOEVSLQWPNFNLNSWEDFVELNGTVHCENENSSLOEDNSAATHIPVLVPVN	919
Qy	928	MWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLQORSLPISLVLPVRINQTVIWDPR	987
Db	920	ILTKEQENSTLYISFTPKGPKTQVQHVQYV-----RIQPSAYDHNMT-LEALVGPVRP	973
Qy	988	Q-----VTFSENLS-----TCHTKE-RUPSHSDFLAELRKAPVNVCSIAVCQRIQCDIPFF	1038
Db	974	HSEDLIITYTWSVQTDPLVTCHSDLKEPSSB---AEQPCPLPGV-----QPRCPVIFV-	1021
Qy	1039	GIOEENFATLKNLSFDWYIKTSHNHLIIVSTAIEILDNSVFULLPGQAFVRSQETKV	1098
Db	1022	--RWEILLQVGTVELSEIKAS-STLJSCSLSVSNFSKHFHYGSKA-SRAQVLKV	1077
Qy	1099	EPFEVNPPLPIVGGSSVGGLLLLLALITAYLYKGFQRQYKDMV-SGGGPPGAP	1152
Db	1078	DLIHEKMLHVYVLSGIGGLVLLPLIYALYKVGFFKRLKEKMEADGVNGSP	1132

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OM protein - protein search, using sw model

Run on: January 13, 2005, 14:59:41 ; Search time 215.571 Seconds
(without alignments)
1918.696 Million cell updates/sec

Title: RWULB-A
Perfect score: 5953
Sequence: 1 MALRVLLTALTLCGFNLD.....FKRQYKMMSEGGPGABPQ 1153

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5953	100.0	1153	2	AAW65090 Human Bet
2	5953	100.0	1153	3	AAW65090 Human CD1
3	5953	100.0	1153	5	AAU80252 Human Int
4	5953	100.0	1153	5	ABG61469 Human Bet
5	5953	100.0	1153	5	AAO14428 Integrin
6	5953	100.0	1153	7	ADP25615 Binding d
7	5943	99.8	1153	2	AAO4136 Alpha sub
8	5937.5	99.7	1152	8	ADM99589 Human Int
9	5930.5	99.6	1152	8	ADP12435 Protein e
10	3514	59.0	1163	8	ADP44061 Human CD1
11	3500	58.8	1163	8	ADN02004 Human inf
12	3500	58.8	1163	8	ADQ17510 Human sof
13	3491	58.6	1163	2	AAO07120 p150.95 a
14	3477	58.4	1163	2	AAW65091 Human Bet
15	3477	58.4	1163	3	AAO07361 Human CD1
16	3477	58.4	1163	5	ABG61470 Human Bet
17	3475	58.4	1163	6	ABU07406 Protein d
18	3475	58.4	1163	7	ADG32005 Human hom
19	3452	58.0	1161	2	AAW78166 Human bet
20	3452	58.0	1161	2	AAW23049 Human bet
21	3452	58.0	1161	2	AAW57491 Human bet
22	3452	58.0	1161	2	AAW65089 Human Bet
23	3452	58.0	1161	2	AAW72825 Human alp
24	3452	58.0	1161	2	AAW73342 Human alp
25	3452	58.0	1161	3	AAW07359 Human alp

ALIGNMENTS

RESULT 1
AAW65090
ID AAW65090 standard; protein; 1153 AA.

AC AAW65090;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human Beta-integrin CD11b subunit protein.
XX
KW Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
KW type-1 diabetes; atherosclerosis; multiple sclerosis; asthma;
KW lung inflammation; acute respiratory distress syndrome; CD11b subunit;
KW rheumatoid arthritis.

OS Homo sapiens.
XX
PN US5728533-A.
XX
PD 17-MAR-1998.
XX
PF 07-JUN-1995; 95US-00485618.
XX
PR 23-DEC-1993; 93US-00173497.
PR 05-AUG-1994; 94US-00286889.
PR 21-DEC-1994; 94US-00362652.
XX
PA (ICOS-) ICOS CORP.
XX
PI Van Der Vieren M, Gallatin WM;
XX
PS WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-1 diabetes.
Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
CC and rheumatoid arthritis
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRVLLTALTLCHGNLDENAMTFQENARFGQSVVLOGSRVVVGAPOEIVAAQR	60
DB	1	MALRVLLTALTLCHGNLDENAMTFQENARFGQSVVLOGSRVVVGAPOEIVAAQR	60
QY	61	GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQALLACGPTVHOTCSNTYVK	120
DB	61	GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQALLACGPTVHOTCSNTYVK	120
QY	121	GLCFIFGNLRQOPQKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL	180
DB	121	GLCFIFGNLRQOPQKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL	180
QY	181	KSKKTLFSLMOYSEEFRIHFTKFEQNNPNRSLVKPIITOLLGRTHATGIRKVVRELFN	240
DB	181	KSKKTLFSLMOYSEEFRIHFTKFEQNNPNRSLVKPIITOLLGRTHATGIRKVVRELFN	240
QY	241	ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFRSEKSRQEL	300
DB	241	ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFRSEKSRQEL	300
QY	301	NTIASKPRDRHVQVNNPEALKTIQNLREKPAIEGTQTSSSSFEHMGQEGFSAIT	360
DB	301	NTIASKPRDRHVQVNNPEALKTIQNLREKPAIEGTQTSSSSFEHMGQEGFSAIT	360
QY	361	SNGPLLSTVGSVDMAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAIILNRVQSLV	420
DB	361	SNGPLLSTVGSVDMAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAIILNRVQSLV	420
QY	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLIGAP	480
DB	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLIGAP	480
QY	481	HYEOTRGQGVSVCPPLRGORARWOCDAVLIGEQQPWGRFGAALTIVLDVNGDKLTQVA	540
DB	481	HYEOTRGQGVSVCPPLRGORARWOCDAVLIGEQQPWGRFGAALTIVLDVNGDKLTQVA	540
QY	541	IGAPGEEDNRGAVYLFHGTSGSISPSHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV	600
DB	541	IGAPGEEDNRGAVYLFHGTSGSISPSHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV	600
QY	601	DLTVAQGHVLLRLSQPVLRVKAIMEFNPREVARNVFECDNQVVKGEAGEVRVCLHVQK	660
DB	601	DLTVAQGHVLLRLSQPVLRVKAIMEFNPREVARNVFECDNQVVKGEAGEVRVCLHVQK	660
QY	661	STRDLREGQIQSVVYTDALDSGRPHRAVNETKSNTRQOTQVLGLTQTCETLKULQP	720
DB	661	STRDLREGQIQSVVYTDALDSGRPHRAVNETKSNTRQOTQVLGLTQTCETLKULQP	720
QY	721	NCIEDPVPPIVLRNLSVGTPLSAFGLNRPVLAEADQRLFTALPPFEKNGCNDNICODD	780
DB	721	NCIEDPVPPIVLRNLSVGTPLSAFGLNRPVLAEADQRLFTALPPFEKNGCNDNICODD	780
QY	781	LSITFSFMSLDCVLVGGPREFNTVTVRNDGEDSYRTQVTFPPDLDSYRKVSTLQNRQ	840
DB	781	LSITFSFMSLDCVLVGGPREFNTVTVRNDGEDSYRTQVTFPPDLDSYRKVSTLQNRQ	840
QY	841	QSRNLACESASSTEVSGALKSTSCINHPFEPENSEVTFNITFDVDSKASLGNKLLKA	900
DB	841	QSRNLACESASSTEVSGALKSTSCINHPFEPENSEVTFNITFDVDSKASLGNKLLKA	900
QY	901	NVTSENNNPRNTKTEFOLELPKVAVMVMTVSHGVSTKYLNFNTASNTSRVWQHOYQVSN	960
DB	901	NVTSENNNPRNTKTEFOLELPKVAVMVMTVSHGVSTKYLNFNTASNTSRVWQHOYQVSN	960

QY	961	LGQSLPISLVFLVPVRLNQTWIDRPOVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV	1020
DB	961	LGQSLPISLVFLVPVRLNQTWIDRPOVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV	1020
QY	1021	VNCSTIACVQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLILVSTABILFNDVSF	1080
DB	1021	VNCSTIACVQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLILVSTABILFNDVSF	1080
QY	1081	TLLPCQGAFAVSQETKVEPEVNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKD	1140
DB	1081	TLLPCQGAFAVSQETKVEPEVNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKD	1140
QY	1141	MWSEGGPPGAEPQ 1153	
DB	1141	MWSEGGPPGAEPQ 1153	

RESULT 2
AAB07360

ID AAB07360 standard; protein; 1153 AA.

XX AAB07360;

XX AC AAB07360;

XX DT 17-JAN-2001 (first entry)

XX XX Human CD11b protein sequence.

XX DE Human; macrophage infiltration inhibition; alpha_d integrin;

XX KW leukocyte integrin; Leu-CAM; leukointegrin; immune response;

XX KW inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;

XX KW atherosclerosis; multiple sclerosis; asthma; psoriasis; Crohn's disease;

XX KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;

XX KW rheumatoid arthritis; central nervous system injury; CD11b.

XX OS Homo sapiens.

XX PN WO200029446-A1.

XX PD 25-MAY-2000.

XX XX 16-NOV-1999; 99WO-US027139.

XX PF 16-NOV-1998; 98US-00193043.

XX PR 08-JUL-1999; 99US-00350259.

XX XX (ICOS-) ICOS CORP.

XX PA Gallatin MW, Van Der Vieren M;

XX PI WPI; 2000-387751/33.

XX DR Use of novel anti-alpha integrin d monoclonal antibodies to inhibit

XX PT macrophage infiltration and reduce inflammation at central nervous system

XX PT injury sites.

XX PS Example 5; Fig 1; 270pp; English.

XX XX Integrins are a class of membrane-associated molecules that participate
CC in cellular adhesion. Integrins are made up of an alpha subunit and a
CC beta subunit. One class of human integrins are restricted to expression
CC in white blood cells and have a common beta2 subunit: the leukocyte
CC integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins
CC have an important role in immune and inflammatory responses. The present
CC protein sequence is the human integrin alpha subunit CD11b. This sequence
CC was used in an alignment to identify a novel beta2 integrin alpha
CC subunit: alpha_d (AAA60014 and AAB07359). The present sequence has
CC approximately 60% identity to the protein sequence of alpha_d. The
CC Alpha_d gene and protein may be useful in therapy for diseases linked to
CC aberrant alpha_d function e.g. Type I diabetes, atherosclerosis, multiple
CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory
CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency
CC (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the

CC inhibition of macrophage infiltration at the site of a central nervous
CC system injury. The monoclonal antibodies can also be used to detect and
CC diagnose Crohn's disease
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 3; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRLLLTALTLCHGFNLDENAMTFQENARGFCQSVVQLQSGRVVVGAPQEIIVAAQR 60
DB 1 MALRLLLTALTLCHGFNLDENAMTFQENARGFCQSVVQLQSGRVVVGAPQEIIVAAQR 60

QY 61 GSYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQQLACGPTVHQTCSNTYVK 120
DB 61 GSYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQQLACGPTVHQTCSNTYVK 120

QY 121 GLCFLFGNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180
DB 121 GLCFLFGNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180

QY 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITOLLGRTHATGIRKVVRELPN 240
DB 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITOLLGRTHATGIRKVVRELPN 240

QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300

QY 301 NTIASKPRDRHVQNNPEALKTIONQREKXPALEGQTQSGSSSFEHEMSQEGFSAAIT 360
DB 301 NTIASKPRDRHVQNNPEALKTIONQREKXPALEGQTQSGSSSFEHEMSQEGFSAAIT 360

QY 361 SNGPLSTVGSYDAGGVPLTYSKEKSTFINNTRVDSMDNDAYLGAAIILNRVQSIV 420
DB 361 SNGPLSTVGSYDAGGVPLTYSKEKSTFINNTRVDSMDNDAYLGAAIILNRVQSIV 420

QY 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480

QY 481 HYEOTRGQSVSCPLPRGQARWOCDAVLGEGQCPWGRFGAALTIVLDVNGDKLTDVA 540
DB 481 HYEOTRGQSVSCPLPRGQARWOCDAVLGEGQCPWGRFGAALTIVLDVNGDKLTDVA 540

QY 541 IGAPGEENRGAVALPHGTSGSISPSHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
DB 541 IGAPGEENRGAVALPHGTSGSISPSHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600

QY 601 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
DB 601 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660

QY 661 STRDLREGQISQVVTYDIALDSGRPHSAVNETKNSTRQTQVLGTQTCTETLKQLP 720
DB 661 STRDLREGQISQVVTYDIALDSGRPHSAVNETKNSTRQTQVLGTQTCTETLKQLP 720

QY 721 NCIEDPVSPVLRNLFSLVGTPLSAFNLRLPVLAEQAORLFTALPFEKNCNDNICODD 780
DB 721 NCIEDPVSPVLRNLFSLVGTPLSAFNLRLPVLAEQAORLFTALPFEKNCNDNICODD 780

QY 781 LSITPSFMSLDCLVVGGPREFNVTVTRNDGDSYRTQVTFPPDLDSYRKVSTLQNRS 840
DB 781 LSITPSFMSLDCLVVGGPREFNVTVTRNDGDSYRTQVTFPPDLDSYRKVSTLQNRS 840

QY 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
DB 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900

QY 901 NVTSENMPRTNKTFFOLELPVKYAVYVMTVSHGVSTKYLNFNTASENTRVQHQYQVSN 960
DB 901 NVTSENMPRTNKTFFOLELPVKYAVYVMTVSHGVSTKYLNFNTASENTRVQHQYQVSN 960

QY 961 LGQSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020
DB 961 LGQSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020

QY 1021 VNCISIAVCORIQCIPPFQIOEEFNATLKGNSLSPDWYIKTSHNHLIIYSTAEILFNDVSF 1080
DB 1021 VNCISIAVCORIQCIPPFQIOEEFNATLKGNSLSPDWYIKTSHNHLIIYSTAEILFNDVSF 1080

QY 1081 TLLPQOGAFVRSQETKVEPEVPNPPLIIVGSSVGGLLALLALITAAALYKLGFFKQYKD 1140
DB 1081 TLLPQOGAFVRSQETKVEPEVPNPPLIIVGSSVGGLLALLALITAAALYKLGFFKQYKD 1140

QY 1141 MMSEGGPPGAPQ 1153
DB 1141 MMSEGGPPGAPQ 1153

RESULT 3
AAU80252
ID AAU80252 standard; protein; 1153 AA.
XX
AC AAU80252;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human integrin 1 alpha-M subunit protein.
XX
KW Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;
KW inflammatory disease; autoimmune disorder; Crohn's disease;
KW human immunodeficiency virus; HIV; myocardial infarction;
KW Sjorgen's syndrome; rheumatoid arthritis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 499..500 /note= "Encoded by GGG CAG AGG"
FT
XX WO200218583-A2.
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027227.
XX
XX 01-SEP-2000; 2000US-0229700P.
XX
XX (BLOO-) CENT BLOOD RES INC.
XX
XX Springer TA, Shimoaka M, Lu C;
XX WPI; 2002-382964/41.
XX N-PSDB; ABSK50046.
XX
XX Modified integrin-I or integrin I-like domain polypeptide useful as an
XX immunogen to produce antibodies specific to polypeptide, comprises a
XX disulfide bond such that polypeptide is stabilized in a desired
XX conformation.
XX
XX Disclosure; Page 109-112; 112pp; English.
XX
XX This invention relates to a modified integrin-I or integrin I-like domain
XX polypeptide comprising at least one disulfide bond so that the domain is
XX stabilised in a desired conformation. The polypeptide of the invention
XX may have antiinflammatory or immunosuppressive activities. The
XX polypeptides of the invention have an open conformation and are useful as
XX immunogens to produce antibodies that selectively bind to integrin I-
XX domain; and for identifying a modulator of integrin activity, or of
XX interaction of an integrin and a cognate ligand. The polypeptide of the
XX invention, or antibodies (preferably anti-LFA-1 antibody) is useful for
XX treating or preventing an integrin mediated disorder which is an
XX inflammatory or autoimmune disorder in a subject and for inhibiting the
XX binding of an integrin to a cognate ligand such as Crohn's disease,

nephritis; human immunodeficiency virus (HIV), myocardial infarction, Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-1 alpha-M protein subunit used to generate the mutant polypeptides of the invention

CC
XX
SQ

Query Match 100.0%; Score 5953; DB 5; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCHGFNLDLTENAMTFQENARGFGQSVVQLGSRVVVGAQEIIVAAQR 60
DB 1 MALRVLLLTALTLCHGFNLDLTENAMTFQENARGFGQSVVQLGSRVVVGAQEIIVAAQR 60
QY 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVK 120
DB 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFGNLRQOPKQPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQL 180
DB 121 GLCFLFGNLRQOPKQPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQL 180
QY 181 KSKTFLSLMOYSEBFRTHFTKBPQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN 240
DB 181 KSKTFLSLMOYSEBFRTHFTKBPQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVDAPFRSKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVDAPFRSKSRQEL 300
QY 301 NTIASKPRDRHVQNNFEALKTIONQUREKXFAIEGTQTGSSSSFEHMGQEGFSAIT 360
DB 301 NTIASKPRDRHVQNNFEALKTIONQUREKXFAIEGTQTGSSSSFEHMGQEGFSAIT 360
QY 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINTRVDSMDNAYLGYAAAILRNRVQSLV 420
DB 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINTRVDSMDNAYLGYAAAILRNRVQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYEOTRGGOVSVCPLPRGQARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYYEOTRGGOVSVCPLPRGQARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPCEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLSGGQDLTMDGLV 600
DB 541 IGAPCEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLSGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKREAGEVRVCLHVQK 660
DB 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKREAGEVRVCLHVQK 660
QY 661 STRDLREGQIOSVVTYDIALDSGRPHSRVAFNETKSTRQTOVLGLTQCETLKLQLP 720
DB 661 STRDLREGQIOSVVTYDIALDSGRPHSRVAFNETKSTRQTOVLGLTQCETLKLQLP 720
QY 721 NCIEDPVSPIVLRNLSFVLGTPLSAFGNLRPLVLAEDAQRLEFALFPPEKNGCNDNICDD 780
DB 721 NCIEDPVSPIVLRNLSFVLGTPLSAFGNLRPLVLAEDAQRLEFALFPPEKNGCNDNICDD 780
QY 781 LSITFSFMSLDCLVVGPREFNVTVVRNDEGDSYRQVTFPPFLDLSYRKVSTLQNORS 840
DB 781 LSITFSFMSLDCLVVGPREFNVTVVRNDEGDSYRQVTFPPFLDLSYRKVSTLQNORS 840
QY 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASIGNKLLKA 900

DB 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASIGNKLLKA 900
QY 901 NVTSENMMPRNTKTEFQLELPVKYAVVMVTSHGVSHTKYNLFTASENTRVMQHQYQVSN 960
DB 901 NVTSENMMPRNTKTEFQLELPVKYAVVMVTSHGVSHTKYNLFTASENTRVMQHQYQVSN 960
QY 961 LGQRSPLISLVLPVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
DB 961 LGQRSPLISLVLPVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
QY 1021 VNCISAVCQRIQCDIPFFGIQEEFNATLKGNSLFDWIKTSHNHLIIIVSTAELLFNDVSF 1080
DB 1021 VNCISAVCQRIQCDIPFFGIQEEFNATLKGNSLFDWIKTSHNHLIIIVSTAELLFNDVSF 1080
QY 1081 TLLPGQAGFVRSQTFETKVEPEVPNPPLIIVGSSVGGLLIILALITAAALYKLGFFKRYKD 1140
DB 1081 TLLPGQAGFVRSQTFETKVEPEVPNPPLIIVGSSVGGLLIILALITAAALYKLGFFKRYKD 1140
QY 1141 MWSEGGPPGAEPPQ 1153
DB 1141 MWSEGGPPGAEPPQ 1153

RESULT 4
ABG61469
ID ABG61469 standard; protein; 1153 AA.
XX
AC ABG61469;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human Beta2 integrin alphaCD11b subunit.
XX
KW Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
XX
OS Homo sapiens.
XX
FN WO200230980-A2.
XX
PD 18-APR-2002.
XX
PF 15-OCT-2001; 2001WO-US032059.
XX
PR 13-OCT-2000; 2000US-00688307.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gallatin WM, Van Der Vieren M;
XX
DR WPI; 2002-463260/49.
XX
PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
FT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
FT limiting autonomic and sensory dysfunction following spinal cord injury.
XX
PS Example 5; Page 191-194; 270pp; English.
XX
CC The invention relates to promoting locomotor recovery, inhibiting
CC locomotor damage, limiting locomotor impairment, or limiting autonomic
CC and sensory dysfunction following spinal cord injury by administering an
CC anti-alpha-d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
CC spinal cord injury victim. The method also involves the use of a ligand
CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
CC vascular cell adhesion molecule). The method is useful for promoting
CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
CC impairment, or limiting autonomic and sensory dysfunction following

CC spinal cord injury. In particular, the spinal cord injury comprises
CC compression of the spinal cord. The antibodies are also useful for
CC reducing inflammation at the site of a central nervous system injury. The
CC specification also details the identification of Beta2 integrin alpha
CC cDNAs and proteins, for use in raising the antibodies. Beta2 integrins
CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
CC colitis, immune complex alveolitis and leukaemia. The present sequence is
CC a Beta2 integrin alpha subunit sequence included for comparison with the
CC Beta2 integrin alpha protein sequences
XX
XX Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 5; Length 1153;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGGQSVVQLQGRVVVGAPOEIVANQR 60
Db 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGGQSVVQLQGRVVVGAPOEIVANQR 60

Qy 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPOLLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPOLLACGPTVHQTCSNTYVK 120

Qy 121 GLCFLFGNLQQQPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180
Db 121 GLCFLFGNLQQQPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180

Qy 181 KKSITLSLMQYSEFRTHFTFKFQNNPNSLVKPTITLLGRTHATGIRKVVRELFN 240
Db 181 KKSITLSLMQYSEFRTHFTFKFQNNPNSLVKPTITLLGRTHATGIRKVVRELFN 240

Qy 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQEL 300

Qy 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTQTGSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTQTGSSSFEHMSQEGFSAAIT 360

Qy 361 SNGPLSTVGSYDAGGVPYLSKEKSTFINMTRVDSMDNAYLGAAIILRNVRQSLV 420
Db 361 SNGPLSTVGSYDAGGVPYLSKEKSTFINMTRVDSMDNAYLGAAIILRNVRQSLV 420

Qy 421 LGAPRYQHIGLVAMPQNTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
Db 421 LGAPRYQHIGLVAMPQNTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAP 480

Qy 481 HYYEQTRGGQVSVCPPLPRGQARWQCDVLYGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYEQTRGGQVSVCPPLPRGQARWQCDVLYGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540

Qy 541 IGAPGEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600

Qy 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPECNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPECNDQVVKGEAGEVRVCLHVQK 660

Qy 661 STRDLREGQIQSVVYTDALDGRPHSRAVFNETKNSRRQTQVLGLTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVVYTDALDGRPHSRAVFNETKNSRRQTQVLGLTQTCETLKLQLP 720

Qy 721 NCIEDPVPVILRLNFSLVGTPLSAFLGNLRPVLAEADAORLFTALPPFKNGCNDNICODD 780
Db 721 NCIEDPVPVILRLNFSLVGTPLSAFLGNLRPVLAEADAORLFTALPPFKNGCNDNICODD 780

Qy 781 LSITFSFMSLCLVVGGRPREFNVTVTVRNDGEDSVRTQVTFEFPPLDLSYRKVSTLQNGRS 840
Db 781 LSITFSFMSLCLVVGGRPREFNVTVTVRNDGEDSVRTQVTFEFPPLDLSYRKVSTLQNGRS 840

Qy 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900
Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900

Qy 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSTKYLNFTASENTRVWQHVOYQVSN 960
Db 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSTKYLNFTASENTRVWQHVOYQVSN 960

Qy 961 LQORSLPISLVFLVPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSSHSDFLAELRKAPV 1020
Db 961 LQORSLPISLVFLVPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSSHSDFLAELRKAPV 1020

Qy 1021 VNCISAVCQRIQCDIPFFGIOEENFATLKGNSLSDWYIKTSHNHLIIYSTABILFNDVSF 1080
Db 1021 VNCISAVCQRIQCDIPFFGIOEENFATLKGNSLSDWYIKTSHNHLIIYSTABILFNDVSF 1080

Qy 1081 TLLPGQGAFAVRSQETKVEPFEVNPPLPLIYGVSSVGGLLLLALITAAALYKLGFFKQYKD 1140
Db 1081 TLLPGQGAFAVRSQETKVEPFEVNPPLPLIYGVSSVGGLLLLALITAAALYKLGFFKQYKD 1140

Qy 1141 MWSEGGPPGAEPQ 1153
Db 1141 MWSEGGPPGAEPQ 1153

RESULT 5
AA014428
ID AA014428 standard; protein; 1153 AA.
XX AA014428;
AC AA014428;
DT 03-MAY-2002 (first entry)
XX Integrin Mac-1 alpha subunit.
DE Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
XX open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.
XX Unidentified.
OS WO200204521-A2.
XX 17-JAN-2002.
PD 09-JUL-2001; 2001WO-US021805.
XX 07-JUL-2000; 2000US-0216600P.
PF (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX (BLOO-) CENT BLOOD RES.
PI Springer T;
XX WPI; 2002-148167/19.
XX New integrin I domain protein having alteration in at least 2
PT noncontiguous regions and exits in an open conformation, useful for
PT treating, preventing or suppressing inflammatory or immunological
PT disorders.
XX Example 1; Fig 1F; 90pp; English.
PS The invention comprises structurally biased variant integrin inserted (I)
XX domain proteins, wherein the alterations to the protein occur in at least
CC two noncontiguous regions. Specifically the variant integrin I domain
CC proteins are structurally biased to exist in the open conformation.
CC thereby altering the binding ability of the protein. The invention also
CC comprises nucleic acids encoding the variant integrin I domain proteins.

CC The integrin I domain proteins and nucleic acids are useful for treating,
CC preventing or suppressing integrin related inflammatory and immunological
CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain
CC proteins and nucleic acids can also be used for treating: ischaemia/
CC reperfusion (e.g. hypovolemic shock), infarction; cerebral shock; viral
CC infection; and cancer. The variant integrin I domain nucleic acids and
CC proteins may be used in gene therapy, as vaccines and to screen for
CC bioactive agents. The present amino acid sequence represents the Mac-1
CC alpha subunit of integrin
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 5; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGGQSVVQLQGRVVVVGAPQEIIVANQR 60
Db 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGGQSVVQLQGRVVVVGAPQEIIVANQR 60
Qy 61 GSLVQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTYVK 120
Db 61 GSLVQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTYVK 120
Qy 121 GLCFLFGSLNRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQL 180
Db 121 GLCFLFGSLNRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQL 180
Qy 181 KSKTSLFSLMYSSEFRHFTHFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Db 181 KSKTSLFSLMYSSEFRHFTHFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Qy 241 ITNGARKNAFKILVITDGEFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
Qy 301 NTIASKPRDRHVFQVNNPEALKTIQNLREKXFAIEGTQTGSSSFHEHMSQEGFSAIT 360
Db 301 NTIASKPRDRHVFQVNNPEALKTIQNLREKXFAIEGTQTGSSSFHEHMSQEGFSAIT 360
Qy 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINMTVRVDSMDNDAYLYGAAIILNRVQSLV 420
Db 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINMTVRVDSMDNDAYLYGAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTOIGAYFGASCLSDVDNSNGSTDVLVIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTOIGAYFGASCLSDVDNSNGSTDVLVIGAP 480
Qy 481 HYYEQTRGGQVSVCPPLPRGQARWQCDALVYGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYEQTRGGQVSVCPPLPRGQARWQCDALVYGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPGEEDNRGANVLFHGTSGSGISPSHSQRIAGSKLSPRLOYFGOSLSGGQDITMDGLV 600
Db 541 IGAPGEEDNRGANVLFHGTSGSGISPSHSQRIAGSKLSPRLOYFGOSLSGGQDITMDGLV 600
Qy 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPCNDQVVKREAGVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPCNDQVVKREAGVRVCLHVQK 660
Qy 661 STRDLREGQIQSVVYTDALDLSGRPHSRVAFNETKNSRQTQVLGLTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVVYTDALDLSGRPHSRVAFNETKNSRQTQVLGLTQTCETLKLQLP 720
Qy 721 NCIEDPSPVILRLNFSLVGTPLSAFGNLRVLAEDAQRLETFALPPEKNCNDNI CODD 780
Db 721 NCIEDPSPVILRLNFSLVGTPLSAFGNLRVLAEDAQRLETFALPPEKNCNDNI CODD 780
Qy 781 LSIITFSFMSLDCLVVGGRPREFNVTVVNDGEDSYRTQVTPFFPLDLSYRKVSTLQNRS 840
Db 781 LSIITFSFMSLDCLVVGGRPREFNVTVVNDGEDSYRTQVTPFFPLDLSYRKVSTLQNRS 840
Qy 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900

Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Qy 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSKYLNFTASENTRVWQHOYQVSN 960
Db 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSKYLNFTASENTRVWQHOYQVSN 960
Qy 961 LQQRSLPTSLVFLVPLVRLNQTVIWDPRQVTFPSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020
Db 961 LQQRSLPTSLVFLVPLVRLNQTVIWDPRQVTFPSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020
Qy 1021 VNCISAVCQRIQCDIPFFGIOEENATLKGNSLDWIKTSHNHLIVSTAEILLFNDSVP 1080
Db 1021 VNCISAVCQRIQCDIPFFGIOEENATLKGNSLDWIKTSHNHLIVSTAEILLFNDSVP 1080
Qy 1081 TLLPGQAGFVRSQETKVEPEVPNPPLIVGSSVGGLLLLALITAAALYKLGFFKROYKD 1140
Db 1081 TLLPGQAGFVRSQETKVEPEVPNPPLIVGSSVGGLLLLALITAAALYKLGFFKROYKD 1140
Qy 1141 MMSEGGPPGAPQ 1153
Db 1141 MMSEGGPPGAPQ 1153
RESULT 6
ADD25615
ID ADD25615 standard; protein; 1153 AA.
XX
AC ADD25615;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #85.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antichyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW rheumatoid arthritis; B-cell disorder; melanoma; carcinoma; sarcoma;
KW malignant condition; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENE-CRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
XX WPI; 2003-801317/75.
DR
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 176; 157pp; English.
XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.

XX
 SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 7; Length 1153;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLTLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAAANOR 60
 DB 1 MALRVLTLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAAANOR 60

QY 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPQLLAGPTVHTQCSNTYVK 120
 DB 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPQLLAGPTVHTQCSNTYVK 120

QY 121 GLCFLFGNLRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKFPEVSTMEOQL 180
 DB 121 GLCFLFGNLRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKFPEVSTMEOQL 180

QY 181 KSKTFLSMLQYSEFRTHFTKFPQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
 DB 181 KSKTFLSMLQYSEFRTHFTKFPQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240

QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
 DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300

QY 301 NTIASKPRDRHVQNNFEALKTIQNLREKFAIEGTQGTSSSSFEHMSQEGFSAIT 360
 DB 301 NTIASKPRDRHVQNNFEALKTIQNLREKFAIEGTQGTSSSSFEHMSQEGFSAIT 360

QY 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSQNDAYLGYAAAILLRNVQSIV 420
 DB 361 SNGPLLTSGVSDWAGGVFLYTSKESKSTFINMTRVDSQNDAYLGYAAAILLRNVQSIV 420

QY 421 LGAPRYQHILVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSDTLVLIGAP 480
 DB 421 LGAPRYQHILVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSDTLVLIGAP 480

QY 481 HYEOTRGQSVVCPLPRGQBARWQCDAVLXGEOGPKRGFGAALTVLGDVNGDKLTDDVA 540
 DB 481 HYEOTRGQSVVCPLPRGQBARWQCDAVLXGEOGPKRGFGAALTVLGDVNGDKLTDDVA 540

QY 541 IGAPCEEDNRGAVLFLHGTSGSGISPSHQSRIAGSKLSPLQYFQGSLSGGQDLTMDGLV 600
 DB 541 IGAPCEEDNRGAVLFLHGTSGSGISPSHQSRIAGSKLSPLQYFQGSLSGGQDLTMDGLV 600

QY 601 DLTGVAQGHVLLLSRQSVLRYKAIMFNPREVARNVFCNDQVVGKAGEVRVCLHVQK 660
 DB 601 DLTGVAQGHVLLLSRQSVLRYKAIMFNPREVARNVFCNDQVVGKAGEVRVCLHVQK 660

QY 661 STRDLREGQIQSVVTVYDLALDSGRPHSRVFNFTKSTRTQTVLGLTQTCETIKQLP 720
 DB 661 STRDLREGQIQSVVTVYDLALDSGRPHSRVFNFTKSTRTQTVLGLTQTCETIKQLP 720

QY 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPVLAEADQRLFTALFPFEKNCNDNICODD 780
 DB 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPVLAEADQRLFTALFPFEKNCNDNICODD 780

QY 781 LSITFSFMSLDCLVVGGRPREFNVTVVRNDEDSYRTQVTFPPDLDSLVRKYSTLQNGRS 840
 DB 781 LSITFSFMSLDCLVVGGRPREFNVTVVRNDEDSYRTQVTFPPDLDSLVRKYSTLQNGRS 840

QY 841 QRSWRLACESASTEVSGALKSTSCSINHPIFPENSEVTENITPDVDSKASLGNKLLKA 900
 DB 841 QRSWRLACESASTEVSGALKSTSCSINHPIFPENSEVTENITPDVDSKASLGNKLLKA 900

QY 901 NVTSENMPRTNKTEFQLELPVKYAVVMVTSKYLNTASNTSRVVMHQYQVSN 960
 DB 901 NVTSENMPRTNKTEFQLELPVKYAVVMVTSKYLNTASNTSRVVMHQYQVSN 960

QY 961 LGQSLPISLVLVPLVRNLQTVWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
 DB 961 LGQSLPISLVLVPLVRNLQTVWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020

QY 1021 VNCISAVCORIOCDIPFPGIOEEFNATLKNLSPDWYIKTSHNHLIYSTAELFNDSVF 1080
 DB 1021 VNCISAVCORIOCDIPFPGIOEEFNATLKNLSPDWYIKTSHNHLIYSTAELFNDSVF 1080

QY 1081 TLLPGQAFVRSQETKVEPEVNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKRYKD 1140
 DB 1081 TLLPGQAFVRSQETKVEPEVNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKRYKD 1140

QY 1141 MWSEGGPPGAPQ 1153
 DB 1141 MWSEGGPPGAPQ 1153

RESULT 7
 AAR04136
 ID AAR04136 standard; protein; 1153 AA.
 XX AAR04136;
 AC AAR04136;
 XX 09-SEP-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1990 (first entry)
 XX
 DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
 XX
 KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
 KW non-specific defence system; integrin gene superfamily.
 XX
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Region 1..16
 FT /label= signal_peptide
 FT Modified-site 86..88
 FT /label= putative N-glycosylation site
 FT Modified-site 240..242
 FT /label= putative N-glycosylation site

FT Modified-site 391..393 /label= putative N-glycosylation site
FT Modified-site 469..471 /label= putative N-glycosylation site
FT Modified-site 693..695 /label= putative N-glycosylation site
FT Modified-site 697..699 /label= putative N-glycosylation site
FT Modified-site 735..737 /label= putative N-glycosylation site
FT Modified-site 802..804 /label= putative N-glycosylation site
FT Modified-site 881..883 /label= putative N-glycosylation site
FT Modified-site 901..903 /label= putative N-glycosylation site
FT Modified-site 912..914 /label= putative N-glycosylation site
FT Modified-site 941..943 /label= putative N-glycosylation site
FT Modified-site 947..949 /label= putative N-glycosylation site
FT Modified-site 979..981 /label= putative N-glycosylation site
FT Modified-site 994..996 /label= putative N-glycosylation site
FT Modified-site 1022..1024 /label= putative N-glycosylation site
FT Modified-site 1045..1047 /label= putative N-glycosylation site
FT Modified-site 1051..1053 /label= putative N-glycosylation site
FT Modified-site 1076..1078 /label= putative N-glycosylation site
FT Region 1106..1134 /label= putative_transmembrane_region
XX
XX EP364690-A.
XX
XX 25-APR-1990.
XX
XX 17-AUG-1989; 89EP-00115159.
XX
XX 23-AUG-1988; 88US-00235353.
XX 09-MAR-1989; 89US-00321239.
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Springer TA, Corbi A;
XX WPI; 1990-125938/17.
XX N-PSDB; AAQ04043.
XX
XX New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating
XX inflammation and viral infections, and in diagnosis.
XX
XX Disclosure; Page ?; 3pp; English.
XX
XX Mac-1 alpha subunit is involved in the response to inflammation, i.e.
XX recognition of and migration to sites of inflammation. It also attaches
XX to cellular substrates as part of this function making it useful in
XX visualising endothelial tissue. Mac-1 is a member of the Integrin Gene
XX superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
XX -MAR-2003 to correct PA field.)
XX
XX Revised record issued on 09-SEP-2004 : Correction to feature table key
XX and pages
XX
SQ Sequence 1153 AA;

Query Match 99.8%; Score 5943; DB 2; Length 1153;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1151; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCCHGNLDTENAMTFOENARGQSVVQLQSGSRVVVGAQOEIVAAQR 60
DB 1 MALRVLLLTALTLCCHGNLDTENAMTFOENARGQSVVQLQSGSRVVVGAQOEIVAAQR 60
QY 61 GSLYQCYSTGSCPIRLQVPVEAVNMSLGLSLAATSPPOLLAGCPTVHQTCSNTYVK 120
DB 61 GSLYQCYSTGSCPIRLQVPVEAVNMSLGLSLAATSPPOLLAGCPTVHQTCSNTYVK 120
QY 121 GLCFPGSNLRQOPKEPEALRGCPQEDSDIAFLIDGSGSLPHDFRMKEFVSTVMEQL 180
DB 121 GLCFPGSNLRQOPKEPEALRGCPQEDSDIAFLIDGSGSLPHDFRMKEFVSTVMEQL 180
QY 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
DB 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVDAPRSEKSOEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVDAPRSEKSOEL 300
QY 301 NTIASKPPDRHVOVNNFEALKTIONOLREKXFAIEGTOTGSSSFHEHMQEFSAAIT 360
DB 301 NTIASKPPDRHVOVNNFEALKTIONOLREKXFAIEGTOTGSSSFHEHMQEFSAAIT 360
QY 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTVRVDSMDNDAYLGYAAAILRNRVQSLV 420
DB 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTVRVDSMDNDAYLGYAAAILRNRVQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
QY 481 HYEOTRGQGVSVCLPRGQARWCCDAVLGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYEOTRGQGVSVCLPRGQARWCCDAVLGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLOQYFGQSLGGQDLTMDGLV 600
DB 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLOQYFGQSLGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVAARVFNFCNDQVVKGEAGEVRVCLHVQK 660
DB 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVAARVFNFCNDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVTVYDLALDSGRPHSRVFNFTKSTRQTOVLGLTQTCETLKLQLP 720
DB 661 STRDLREGQIQSVVTVYDLALDSGRPHSRVFNFTKSTRQTOVLGLTQTCETLKLQLP 720
QY 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPVLAEDAQRFTALFPPEKNCNDNICODD 780
DB 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPVLAEDAQRFTALFPPEKNCNDNICODD 780
QY 781 LSITFSFMSLDCLVVGPREFNVTVVRNDEGDSYRQVTFPPFLDLSYRKVSTLQNR 840
DB 781 LSITFSFMSLDCLVVGPREFNVTVVRNDEGDSYRQVTFPPFLDLSYRKVSTLQNR 840
QY 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASLGNKLLKA 900
DB 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTKEFQLELPVKYAVYVVTSHGVSTKYLNTASNTSRVQMHOQYQVN 960
DB 901 NVTSENMPRTNKTKEFQLELPVKYAVYVVTSHGVSTKYLNTASNTSRVQMHOQYQVN 960
QY 961 LGQSLPISLVFLVPLVRLNQTIVDRPQVTFSENLSTCHTKERLPSSDPLAEURKAPV 1020
DB 961 LGQSLPISLVFLVPLVRLNQTIVDRPQVTFSENLSTCHTKERLPSSDPLAEURKAPV 1020
QY 1021 VNCISAVCORIQCDIPFFGIEEFNATLKGNSLSDWYIKTSHNLLIIVSTAEILFNDVSF 1080
DB 1021 VNCISAVCORIQCDIPFFGIEEFNATLKGNSLSDWYIKTSHNLLIIVSTAEILFNDVSF 1080

Qy 1081 TLLPCQGAFAVSQSTETKVEPEVPNPPLIVGVSSVGGLLLLALITAAALYKLGFFKRYKD 1140
Db 1081 TLLPCQGAFAVSQSTETKVEPEVPNPPLIVGVSSVGGLLLLALITAAALYKLGFFKRYKD 1140
Qy 1141 MMSGGPPGAPQ 1153
Db 1141 MMSGGPPGAPQ 1153
RESULT 8
ADM99589
ID ADM99589 standard; protein; 1152 AA.
XX ADM99589;
AC ADM99589;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human integrin alphaM subunit precursor protein.
XX
KW integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
KW osteopathic; cytostatic; immunosuppressive; antiinflammatory;
KW neuroprotective; antiskinning; immunotherapy; inflammatory;
KW autoimmune disorder; thrombosis; cancer; osteoporosis;
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
KW alphaM.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 965 /note= "Encoded by CCC"
FT
XX
XX WO2004007530-A2.
XX
XX 22-JAN-2004.
XX
XX 17-JUL-2003; 2003WO-US022301.
XX
XX 17-JUL-2002; 2002US-0396783P.
PR 17-JUL-2002; 2002US-0396790P.
PR 11-SEP-2002; 2002US-0410135P.
XX
XX (BLOO-) CENT BLOOD RES INC.
FA
XX
XX Springer TA, Takagi J;
XX
XX WPI; 2004-122877/12.
DR N-PSDB; ADM99588.
XX
XX Novel modified integrin protein having extracellular domains of integrin
PT alpha and beta subunits or integrin alphaII and beta3 subunit, useful for
PT treating integrin mediated disorders.
XX
XX Disclosure; SEQ ID NO 4; 232pp; English.
XX
XX The invention relates to a novel isolated or recombinant modified
CC integrin protein having extracellular domains of integrin alpha and beta
CC subunits where one of the subunits has one or more mutations, an altered
CC surface feature or an amino acid substitution or internal deletion,
CC extracellular domains of the integrin beta subunit that comprise a
CC mutation that alters a non-cysteine residue to cysteine or extracellular
CC domains of integrin alpha and beta subunits. The polypeptide of the
CC invention demonstrates antipsoriatic, thrombolytic, anticoagulant,
CC osteopathic, cytostatic, immunosuppressive, antiinflammatory,
CC neuroprotective and antiskinning activities and may be useful for
CC immunotherapy in order to prevent or treat an integrin-mediated disorder
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
CC sclerosis. The current sequence is that of the human integrin alphaM
CC subunit precursor protein of the invention.
XX
XX Sequence 1152 AA;

Query Match 99.7%; Score 5937.5; DB 8; Length 1152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1151; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MALRVLLLTALTLCCHGNLDTENAMTFOENARGFGQSVVQLQGSVVVGAQOEIVAAQR 60
Db 1 MALRVLLLTALTLCCHGNLDTENAMTFOENARGFGQSVVQLQGSVVVGAQOEIVAAQR 60
Qy 61 GSLYQCDYSTGSCPEIRLQVPEAVNMSLGLSLAATSPQQLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGSCPEIRLQVPEAVNMSLGLSLAATSPQQLACGPTVHQTCSNTYVK 120
Qy 121 GLCFPGSNLRQOKPPEALRGCPQEDSDTAFLIDSGSIIIPHDPRMKEFVSTVMEQL 180
Db 121 GLCFPGSNLRQOKPPEALRGCPQEDSDTAFLIDSGSIIIPHDPRMKEFVSTVMEQL 180
Qy 181 KKSXTLFSLMQYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
Db 181 KKSXTLFSLMQYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300
Qy 301 NTIASKPRDRHVQVNNFEALKTIONQLREKXPALEGTOGTGSSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPRDRHVQVNNFEALKTIONQLREKXPALEGTOGTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAAILRNRVQSLV 420
Db 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAAILRNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGQIGAYFGASLCSVDVDSNGSDTLVLIGAP 480
Db 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGQIGAYFGASLCSVDVDSNGSDTLVLIGAP 480
Qy 481 HYEQTTRGGQVSVCPPLPRGQBARWQCDALVIGEQQPMGRFGAALTIVLDVNGDKLTDVA 540
Db 481 HYEQTTRGGQVSVCPPLPRGQBARWQCDALVIGEQQPMGRFGAALTIVLDVNGDKLTDVA 540
Qy 541 IGAPGEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
Qy 661 STRDLREGQIQSVVYDLDLDSGRPHSRVAVNETKSTRQTQVLGLTQTCETIKLQLP 720
Db 661 STRDLREGQIQSVVYDLDLDSGRPHSRVAVNETKSTRQTQVLGLTQTCETIKLQLP 720
Qy 721 NCIEDPVSPVLRNLFSLVGTPLSAFNLRLPVLAEDAORLFTALPFEKNCNDNICODD 780
Db 721 NCIEDPVSPVLRNLFSLVGTPLSAFNLRLPVLAEDAORLFTALPFEKNCNDNICODD 780
Qy 781 LSITFSFMSLCLVVGGRPREFNVTVTRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRK 840
Db 781 LSITFSFMSLCLVVGGRPREFNVTVTRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRK 840
Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGKLLKA 900
Qy 901 NVTSENMPRTNKTKEFQLELPVKYAVVMVTSKYLNFPTASENTSRYVMHOYQVSN 960
Db 901 NVTSENMPRTNKTKEFQLELPVKYAVVMVTSKYLNFPTASENTSRYVMHOYQVSN 960
Qy 961 LGQRLSLPISLFLVPRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDSFLAELRKAPV 1020
Db 961 LGQRLSLPISLFLVPRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDSFLAELRKAPV 1020
Qy 1021 VNCSIAVCQRIQCDDIPFPGIEEFNATLKGNLSDFWYIKTSHNHLIVSTABILFNDSVF 1080

Db 1020 VNCSTAVCQRIQCDIPFFGQIEFNATLKGNSLSEDFWYIKTSHNLLIVSTAAILFNDVSF 1079
 Qy 1081 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
 Db 1080 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1139
 Qy 1141 MMSEGGPPGAEPO 1153
 Db 1140 MMSEGGPPGAEPO 1152

RESULT 9
 ADP12435
 ID ADP12435 standard; protein; 1152 AA.
 XX
 AC ADP12435;
 XX
 DT 12-AUG-2004 (first entry)
 DE
 DE Protein encoded by mRNA of the invention #45.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2444; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 XX
 SQ Sequence 1152 AA;

Query Match 99.6%; Score 5930.5; DB 8; Length 1152;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1150; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MALRVLLLTALTLCHGNLDTENAMTFOENARGQSVVQLQGSRRVVVGAPQEIVAAQR 60
 Db 1 MALRVLLLTALTLCHGNLDTENAMTFOENARGQSVVQLQGSRRVVVGAPQEIVAAQR 60

Qy 61 GSLVQCDYSTSCBPIRLQVPVEAVNMISLGLSLAATTSPPQLLACGPTVHOTCSENTYVK 120
 Db 61 GSLVQCDYSTSCBPIRLQVPVEAVNMISLGLSLAATTSPPQLLACGPTVHOTCSENTYVK 120
 Qy 121 GLCFLFGSNLQOQPKPEALRGCPQEDSDIAFLIDGSGSII PHDFRMRKMFVSTVMQOL 180
 Db 121 GLCFLFGSNLQOQPKPEALRGCPQEDSDIAFLIDGSGSII PHDFRMRKMFVSTVMQOL 180
 Qy 181 KKSKTFLSLMOYSEBFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
 Db 181 KKSKTFLSLMOYSEBFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
 Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVI PEADREGVIRYVIGCVDAFSEKSRQEL 300
 Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVI PEADREGVIRYVIGCVDAFSEKSRQEL 300
 Qy 301 NTIASKPPRDHVFQNNFEALKTIONLRKXKFAIEGTQTGSSSSSFEHMQEGFSAAIT 360
 Db 301 NTIASKPPRDHVFQNNFEALKTIONLRKXKFAIEGTQTGSSSSSFEHMQEGFSAAIT 360
 Qy 361 SNGPILSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIIILNRVQSLV 420
 Db 361 SNGPILSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIIILNRVQSLV 420
 Qy 421 LGAPRYOHIGLVAMFRONTGWNESNANVKGTOIGAYFCASICSVDVDSNGSTDVLIGAP 480
 Db 421 LGAPRYOHIGLVAMFRONTGWNESNANVKGTOIGAYFCASICSVDVDSNGSTDVLIGAP 480
 Qy 481 HYEQTRGGQVSVCPPLPRGQARWQCDAVLYGEOGQPMGRFGAALTVLGDVNGDKLTDVA 540
 Db 481 HYEQTRGGQVSVCPPLPRGQARWQCDAVLYGEOGQPMGRFGAALTVLGDVNGDKLTDVA 540
 Qy 541 IGAPGEDNRCANVLFHGTSGSISPSHSQRIAGSKLSPRLQYFGQSLSGQDITMDGLV 600
 Db 541 IGAPGEDNRCANVLFHGTSGSISPSHSQRIAGSKLSPRLQYFGQSLSGQDITMDGLV 600
 Qy 601 DLTVGAQGHVLLLRSPVLKVAIMEFNPREVARNVECNDDQVVKGEAGVRVCLHVQK 660
 Db 601 DLTVGAQGHVLLLRSPVLKVAIMEFNPREVARNVECNDDQVVKGEAGVRVCLHVQK 660
 Qy 661 STRDLREGQIQSVVTVYDLDLSDGRPHSRVFNSTKSTRQTOVLGLTQTCETLKLQLP 720
 Db 661 STRDLREGQIQSVVTVYDLDLSDGRPHSRVFNSTKSTRQTOVLGLTQTCETLKLQLP 720
 Qy 721 NCIEDPVSPIVLRNFSLVGTPLSAFCNLRPVLAEADAQRLFTALFPPEKNCNDNI CODD 780
 Db 721 NCIEDPVSPIVLRNFSLVGTPLSAFCNLRPVLAEADAQRLFTALFPPEKNCNDNI CODD 780
 Qy 781 LSITFSFMSLDCLVVGPFREFNVTVTVRNDGEDSYRTQVTFPPFDLSYRKVSTLQNRS 840
 Db 781 LSITFSFMSLDCLVVGPFREFNVTVTVRNDGEDSYRTQVTFPPFDLSYRKVSTLQNRS 840
 Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKA 900
 Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKA 900
 Qy 901 NVTSNNMPRTNKTFOLELPVKYAVVMVVTSHGVSTKYLNFTASENTSRVMQHOYQVSN 960
 Db 901 NVTSNNMPRTNKTFOLELPVKYAVVMVVTSHGVSTKYLNFTASENTSRVMQHOYQVSN 960
 Qy 961 LGQRSPISLVFLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
 Db 961 LGQRSPISLVFLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
 Qy 1021 VNCSTAVCQRIQCDIPFFGQIEFNATLKGNSLSEDFWYIKTSHNLLIVSTAAILFNDVSF 1080
 Db 1021 VNCSTAVCQRIQCDIPFFGQIEFNATLKGNSLSEDFWYIKTSHNLLIVSTAAILFNDVSF 1080
 Qy 1081 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
 Db 1081 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140

Qy 1141 MMSGGPPGABPQ 1153
Db 1140 MMSGGPPGABPQ 1152

RESULT 10
ID ADP44061 standard; protein; 1163 AA.
XX AC ADP44061;
XX DT 09-SEP-2004 (first entry)
XX DE Human CD11C protein SEQ ID NO:14.
XX KW HIV entry inhibitor; cell surface protein inhibitor; HIV infection;
XX KW anti-HIV; virucide; HIV uptake inhibitor; human; CD11C; integrin alpha x.
XX OS Homo sapiens.
XX PN WO2004053094-A2.
XX PD 24-JUN-2004.
XX PF 08-DEC-2003; 2003WO-US039208.
XX PR 06-DEC-2002; 2002US-0431522P.
XX PA (PDP-1) PPD DEV LP.
XX PI Dunn SÜ, Holzmayer TA;
XX DR WPI; 2004-480928/45.
XX DR N-PSDB; ADP44060.
XX PT Identifying an inhibitor of human immunodeficiency virus (HIV) entry into
PT a human host cell useful for preventing and/or treating HIV infection, by
PT identifying an inhibitor of a cell surface polypeptide such as CXCR-4.
XX PS Claim 1; SEQ ID NO 14; 133pp; English.
XX CC The present invention describes a method (M1) for identifying an
CC inhibitor of HIV entry into a human host cell. (M1) comprises identifying
CC an inhibitor of a cell surface polypeptide selected from CXCR-4 (352
CC amino acids, SEQ ID NO:8, ADP44055), CCR4 (360 amino acids, SEQ ID NO:10,
CC ADP44057), CCR7 (378 amino acids, SEQ ID NO:12, ADP44059), CD11C (1163
CC amino acids, SEQ ID NO:14, ADP44061), CD47 (323 amino acids, SEQ ID
CC NO:16, ADP44063), CD68 (354 amino acids, SEQ ID NO:18, ADP44065), CD69
CC (199 amino acids, SEQ ID NO:20, ADP44067), CD74 (366 amino acids, SEQ ID
CC NO:22, ADP44069), CSF3R (836 amino acids, SEQ ID NO:24, ADP44071), RARA
CC (462 amino acids, SEQ ID NO:26, ADP44073), GABBR1 (578 amino acids, SEQ
CC ID NO:28, ADP44075), P2X1 (150 amino acids, SEQ ID NO:30, ADP44077),
CC HELO1 (299 amino acids, SEQ ID NO:32, ADP44079), GPRK6 (576 amino acids,
CC SEQ ID NO:34, ADP44081), or PFK2B (1009 amino acids, SEQ ID NO:36,
CC ADP44083). Also described: (1) an inhibitor of a cell surface polypeptide
CC as described above in a human host cell preventing HIV entry into the
CC human host cell; (2) a pharmaceutical composition comprising an inhibitor
CC of (1) and a carrier; and (3) conferring resistance to HIV infection in
CC an individual, by administering the pharmaceutical composition of (2). An
CC inhibitor of HIV entry has anti-HIV and virucide activities, and can be
CC used as an HIV uptake inhibitor. (M1) is useful for identifying
CC protective compounds that inhibit entry of HIV into cells, useful for the
CC prevention and/or treatment of HIV infection. The present sequence
CC represents human integrin alpha x (CD11C), which is used in the
CC exemplification of the present invention.
XX Sequence 1163 AA;

Query Match 59.0%; Score 3514; DB 8; Length 1163;
Best Local Similarity 61.4%; Pred. No. 1.4e-278;
Matches 701; Conservative 139; Mismatches 295; Indels 6; Gaps 4;

Qy 5 VLLLTALTLCHGFLNLTENAMTFQENARGFGQSVVLQGSRRVVGAPQEIIVAAANQSGSLY 64

Db 8 LLLFTALATSLGFLNLTDELTAFRVDSAGFGSDSVVQYANSVVVGAPQKITAANQTGGLY 67
Qy 65 QCDYSTGSCBPIRLQVPVEAVNMSLGLSLAATTSPOLLACGPTVHOTCSENTYVKGLCF 124
Db 68 QCGYSTGACEFGLQVPPEAVNMSLGLSLASTTSPQLLACGPTVHHCGRNMYTGLCF 127
Qy 125 LFGSNLRQOPKQFPPEALRGCPQEDSDIAFLDGGSGSIIPHDFRRMKFVSTVMEQLKSK 184
Db 128 LLGPT--QLTQRLPVSROECPRQEQDIVFLDGGSGSISSRNFAFMNFWRAVISQFORPS 185
Qy 185 TLPQLMQYSEFRTHFTPEFQNNPNRSLVKPITOLLGRTHRTATGIRKVVRELNIYNG 244
Db 186 TQPSLMQFSNKFQTHFTPEEFRRSNPLSLASVHQLQGFYTTATAIQVNVHRLPHASVG 245
Qy 245 ARKNAFKLVITDGEKFGDPLGYEDVPEADREGVIRYGVGDAPFSEKSRQBLNTIA 304
Db 246 ARRAAKLIVITDGKEGSDLYKDVIPMDAAGIIRYAGVGLAFQNRISWKELNDIA 305
Qy 305 SKPPRDHVQVNNFEALKTIQNLREKXFAIEGTQTGSSSFEHMSQEGFSAATISNGP 364
Db 306 SKPSQEHIFKVEDFDALKDIQNLKEKIFAIEGTETTSSSFELEMAQEGFSAVTPDGP 365
Qy 365 LLSTVGSYDWAGCVFLYTSKEKSTFNNTRVDSMDNDAYLGYAAAIILNRVQSLVIGAP 424
Db 366 VLGAVGSTWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGSTELALWKVQSLVLGAP 425
Qy 425 RYQHIGLVAMFRONTMMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYYE 484
Db 426 RYQHTGRAVIFTQVSRQWRKAEVTGTOIGYFGASLCSVDVDSGSTDVLVIGAPHYYE 485
Qy 485 QTRGGQSVCPPLPRGQARWQCDALYGEQGPGRFGAALTVLGDVNGDKLTDVAIGAP 544
Db 486 QTRGGQSVCPPLPRGWR--RWCDAVLYGEQGPGRFGAALTVLGDVNGDKLTDVIGAP 544
Qy 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGSLGGGDLTDGDLVDLTV 604
Db 545 GEENRGAVYLFHGVLGPSISPSHSQRIAGSKLSPRLQYFGQALSGGDLTDGDLVDLAV 604
Qy 605 GAQGHVLLRQSVPLRVKAIEMFNPREVARNVFCNDQVWVGKEAGEVRCVLHVOKSTRD 664
Db 605 GARQVLLRTRFVLWVGVSNOFPAEIPRAFAFECREQVSEQTLVQSNICLYIDKRSKN 664
Qy 665 RLREGQIQSVVYDLDLDSGRPHRAVFNETKNSRTRQTVLGLTQTCETLKLQLPNCIE 724
Db 665 LLSGRDLQSSVTLDLALDPGRSLSPRATFQETKNRSLSRVRLGLKAHCENFNLLPSCVE 724
Qy 725 DPVSPVILNLSLVGTPLSAFGLNLRPLVLAEDAQLFTALPFPEKNCNDNICQDDLSIT 784
Db 725 DSVTPITLRLNFTLVGLKLLAFRLNRLPMLAADAQRYFTASLPFEKNCADHICQDNLGIS 784
Qy 785 FSNLSLCLVVGPREFNVTVVRNDGSDSVRTQVTFPPFLDLSYRKVSTLQNRQSRSM 844
Db 785 FSPFLKSLVLSGNLELNAEVMVWVNDGSDSGTITTFSHPAGLSRYRYAEGQKQQLRSL 844
Qy 845 FLACESASTSEVGALKSTSCSINHPIFENSEVFNITFDVDSKASLGKLLKANVTS 904
Db 845 HLTCDSDAPVG--SQGTSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS 902
Qy 905 ENNPRNTKTFOLELPVKYAVYVMTSHGVSTKVLNFTAS--ENTSRVWQHOYOVSNLQ 963
Db 903 ENNPTKSTTFOLELPVKYAVYVMTSHGVSTKVLNFTAS--ENTSRVWQHOYOVSNLQ 962
Qy 964 RSLPISLVFLVPLRLNQTVMWRPOVTFSENLSTCTHKERLPSHSDFLAEILRKAPVNVN 1023
Db 963 RDLPVSNFVFWPVELNQAEMVMDVEVSHVPQPSLRCSEKTAAPPASDFLAHQKPVLD 1022
Qy 1024 SIACVQRIQCDIPFFGIEEFNATLKGNSLFDWYIKTSHNHLIIVSTAILFNDSVFTLL 1083
Db 1023 SIAGCLRPRCDVPSPVQBELDFTLKGNSLFGWVRQILQKKVSVVSVVAEITFDTSVYSOL 1082
Qy 1084 PQGAFVRSQVETKVEPPEVFNPLPLIYVSSVGGLLILALITALYLYKLGFFKQYKDWMS 1143

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 327.
 XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX OS Homo sapiens.
 XX PN WO2004048938-A2.
 XX PD 10-JUN-2004.
 XX PF 26-NOV-2003; 2003WO-US038193.
 XX PR 26-NOV-2002; 2002US-0429739P.
 XX PA (PROT-) PROTEIN DESIGN LABS INC.
 XX PI Aziz N, Ginsburg WM, Zlotnik A;
 XX DR WPI; 2004-441208/41.
 XX PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX PS Example 2; SEQ ID NO 327; 210pp; English.
 XX CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cyostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX SQ Sequence 1163 AA;
 Query Match 58.8%; Score 3500; DB 8; Length 1163;
 Best Local Similarity 61.3%; Pred. No. 2e-277;
 Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;
 QY 5 VLLTALTLCHGFNLDENAMTFQENARFGQSVVQLQSGRRVVGAPQEIIVAAANQDGLY 64
 DB 8 LLLFTALATSLGFLNLDTELTAFRVDSAGFGDSVVQYANWVVGAPQKITAANQTGGLY 67
 QY 65 QCDYSTGCEPIRLQVPVEANVMSLGLSIAATTSPPOLLACGPTVHQCSENTYVYKLCF 124
 DB 68 QCGYSTGACEPIGLQVPPEANVMSLGLSLASTSPSOLLACGPTVHCEGGRNMYLTGLCF 127
 QY 125 LFGSNLRQOPKFPBALGCGPOEDSDIAFLIDGSGSIIPHPRRMKEFVSTVMEOLKXSK 184
 DB 128 LLGPT--QLTQLPVSRECFQEQDIIVFLIDGSGSISRNFATMNFVRAVISQFQPS 185
 QY 185 TLFLSMQVSEFRIHFTFKGFQNNPNRSLVKPITQLLGRTHATGIRKVRVRELFNITNG 244
 DB 186 TQSLMQFSNKPQTHFTFEFRRTSNPLSLASVHQLQGFYTTATAIQNVHRLPHASVG 245
 QY 245 ARKNAFKILVITDCEKGDPLGYEDVPEADREGVIRYVIGVGDAPRSEKSRQELNTIA 304
 DB 246 ARRDATKILVITDCKGKGDSDYDVTIPMDAAGIIRIYAGVGLAFQNRNWSKELNDIA 305
 QY 305 SKPPRDHVFQNNFALKTIQNLREKXFAIBGTOTGSSSSPEHEMSQEGFAAITSNGP 364
 DB 306 SKPSGEHFKVDFDALLKDQIQNLKEKFAIBGTETTSSTSSFELEMAQEGFSAVTPGP 365
 QY 365 LLSTVGSYDMAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAAIILNRNVQSLVLGAP 424

DB 366 VLGAVGSFTSGGAFLYPPNNMSPFIINNSQBNVMDRDSYLGSTELALWKGVQSLVLGAP 425
 QY 425 RYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAPHYVE 484
 DB 426 RYQHTGKAVIFTQVSRQWRMKAETGTQIGYFGASLCSVDVDTGSDTLVIGAPHYVE 485
 QY 485 QTRGGQSVSVCPLPRGORARWQCDVLYGEOQPMGRFGAALTIVLGDVNGDKLTVDVIGAP 544
 DB 486 QTRGGQSVSVCPLPRGWR--RWCDAVLYGEOQHPWGRFGAALTIVLGDVNGDKLTDVVIGAP 544
 QY 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLSCGGDLTWDGLVDLTV 604
 DB 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLSCGGDLTWDGLVDLAV 604
 QY 605 GAQGHVLLLRQOPVLRVKAIMFENPREVARNVFECNDQVKGKEAGEVRCVLCVHVKSTRD 664
 DB 605 GARGOVLLLRTRPVLWGVGSMQFPAEIPRAFAECREQVSEQTLVQSNICLYIDRKN 664
 QY 665 RLREGQIQSVVYDIALDGRPHSRVFNENETKSTRQTQVLGLTQTCETLKLQLPNCIE 724
 DB 665 LIGSRDLQSSVTLDLALDPGRLSPRATFOETKNRSLSRVRLGLKAHCENFNLLPSCVE 724
 QY 725 DPVSPVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALPFEKNCNCGDNICQDDLSIT 784
 DB 725 DSVTPITLRLNFTLVGKPLLAFLRNLRLPMLAALAQRYFTASLPFEKNCNCGADHICQDNLGIS 784
 QY 785 FSPNSLDCLVVGGPREFNVTVRNDGSDSYRTQVTPFPFLDLSYRKVYSTLQNRQSRSW 844
 DB 785 FSPFLKSLVLVGSNLELNAEYVWVNDGSDSYGTTTFSPHAGLSRYVAGQKQQLKSL 844
 QY 845 RLACESASTSEVGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKANVTS 904
 DB 845 HLTCDSPVGG--SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLTANVSS 902
 QY 905 ENNPRNTKTSFQELPVKYAVYVWVTSYHGVSTKYLNETAS--ENTSRVMOHQYQVSNLQ 963
 DB 903 ENNPRNTKTSFQELPVKYAVYVWVTSYHGVSTKYLNETAS--ENTSRVMOHQYQVSNLQ 962
 QY 964 RSLPISLVPLVRLNQTIVDRPQVTSSENLSTCTCHTKERLPSHSDFLAEURLKAPVNC 1023
 DB 963 RDLVSVINFWVPELVNQAEMVDEVSHQVPSLRCSSEKTAAPPASDFLHAIQKPVLD 1022
 QY 1024 SIACVQRIQCDIPFFGIQEFNATLKGNLSDWIKTSHNHLIIVSTAEILFNDSVFTLL 1083
 DB 1023 SIACVQRIQCDIPFFGIQEFNATLKGNLSDWIKTSHNHLIIVSTAEILFNDSVFTLL 1082
 QY 1084 PQGAFVRSQETKTEKPEPEVNPPLIVGSSVGGLLLLALITAAALYKLGFPKQYKDWMS 1143
 DB 1083 PQGAFVRSQETKTEKPEPEVNPPLIVGSSVGGLLLLALITAAALYKLGFPKQYKDWMS 1142
 QY 1144 E 1144
 DB 1143 E 1143
 RESULT 13
 ID AAR07120 standard; protein; 1163 AA.
 AC AAR07120;
 DT 25-MAR-2003 (revised)
 DT 05-FEB-1991 (first entry)
 DE p150.95 alpha subunit encoded by clone lambda dx47.
 KW p150.95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia;
 KW rhinovirus.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH

FT Region 1..19
 FT /label= signal peptide
 FT Region 20..44
 FT /label= N-terminus
 FT Modified-site 61..63
 FT /label= glycosylation site
 FT Modified-site 89..91
 FT /label= glycosylation site
 FT Modified-site 385..387
 FT /label= glycosylation site
 FT Modified-site 392..394
 FT /label= glycosylation site
 FT Modified-site 697..699
 FT /label= glycosylation site
 FT Modified-site 735..737
 FT /label= glycosylation site
 FT Modified-site 899..901
 FT /label= glycosylation site
 FT Modified-site 904..906
 FT /label= glycosylation site
 FT Modified-site 939..941
 FT /label= glycosylation site
 FT Modified-site 1050..1052
 FT /label= glycosylation site
 FT Domain 1108..1133
 FT /label= transmembrane
 PN WO9010646-A.
 XX
 XX
 PD 20-SEP-1990.
 XX
 XX
 PF 09-MAR-1990; 90WO-US001257.
 XX
 PR 09-MAR-1990; 90WO-US001257.
 XX
 PA (DAND) DANA FARMER CANCER INST INC.
 XX
 PI Corbi AA, Springer TA;
 XX
 DR WPI; 1990-304985/40.
 DR N-PSDB; AAQ06068.
 XX
 XX
 PT Treatment of viral esp. rhino-viral infection - by admin. of alpha sub-unit of p150.95 cell surface adhesion receptor, opt. together with a beta chain of CD-18 family.
 PT
 PS Disclosure; Fig 3; 59pp; English.
 XX
 CC Clone lambda X47 was isolated from a cDNA library constructed from total RNA extracted from phorbol myristate acetate stimulated HL-60 myelomonocytic cells. The library was screened with oligonucleotide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAQ06068, AAR07121-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 1163 AA;
 SQ
 Query Match 58.6%; Score 3491; DB 2; Length 1163;
 Best Local Similarity 61.1%; Pred. No. 1.1e-276;
 Matches 697; Conservative 139; Mismatches 299; Indels 6; Gaps 4;
 QY 5 VLLTALTCLHGNLDTENAMTFOENARGFGQSVVQLQGSVVVVGAPQEIIVANQORSLSY 64
 DB 8 LLLFTLATSIGFNLDEELTAFRVDSAGFSDSVVQVANSVVVVGAPQKITAANQTGGLY 67
 QY 65 QCDYSTGSCPEIRLQVPEAVNMSLGLSLAATTSPOLLACGPTVHOTCSENTYVKGLCF 124
 DB 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLASTTSPQLLACGPTVHHECGENMILTGLCP 127

QY 125 LFGSNLRQOPKQPFALRGCPQEDSDIAFLIDGSGSIIPHPRRMKEFVSTVMEOLKSKS 184
 DB 128 LLGPT--QLTQRLPVSROCEPCQODIVFLIDGSGSISSRNFAFMWNVRAVISQFQPS 185
 QY 185 TLFSLMOYSEEFRIHTFKFQNNPNRSLVKPITQLLGRTHRTATGIRKVVVRELFINNG 244
 DB 186 TQFSLMQPSNKFQHTFEEFRTSNPLSLASVHQLQGFTYTATAIQQVVRHLPHASVG 245
 QY 245 ARKNAFKLIVITDGEKFGDPLGYEDVITPEADRGVRYRVIGVDGAPRSEKSRQELNIA 304
 DB 246 ARDATKILIVITDGEKFGDPLGYEDVITPEADRGVRYRVIGVDGAPRSEKSRQELNIA 305
 QY 305 SKPRDHVQVNNFEALKTIQNLREKXFAFEGTGTGSSSSSEFEHMSDEGSAITSNP 364
 DB 306 SKPQEHIFKVEDFDALKDIONQLEKIFALEGTEHTSSSFELEMAEGESAVFTPGP 365
 QY 365 LLSTVGSYDAGVFLYTSKEKSTFINNTRVDSNDNDAYLGYAAAILNRNVQSLVLGAP 424
 DB 366 VLGAVGSTWGGAFLYPPNMSPTFINNSQENVMDRDSYLSYSELALWKGVSILVLGAP 425
 QY 425 RYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASLCSDVDSDNGSTDLVLIGAPHYYE 484
 DB 426 RYQHTKAVIPTQVSROWMKAEVTGTQISYFGASLCSDVDSDNGSTDLVLIGAPHYYE 485
 QY 485 QTRGGQVSVCPPLRGQARWQCDALYCEQGPWRFGAALTVLGDVNGDKLTDVAIGAP 544
 DB 486 QTRGGQVSVCPPLRGWR--RWCDALYGEQHPWRFGAALTVLGDVNGDKLTDVAIGAP 544
 QY 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQSGSGGQDLTMDGLVDITV 604
 DB 545 GEEENRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQSGSGGQDLTMDGLVDITV 604
 QY 605 GAQGHVLLRSQVPLRVKAMEENPREVARNVFECNDVYKGEAGEVRVCLHVKQSTRD 664
 DB 605 GARGVLLLRTRPVLMVGVSMQFIPAEIPSAFECREQVSEBQTLVQSNICLYIDKSGSN 664
 QY 665 RLREGQIQSVVYTDALDSDGRPHSAFVFNETKSTRQTQVLGTLTQTCETLKLQPNCE 724
 DB 665 LLSRDLQSSVTLDLALDPCRLSPRATFQETKNSLSRVRVLGLKAHCENFNLLPSCVE 724
 QY 725 DPVSPVIRLNFSLVGTPLSAFGLNLRPVLAEDAQRLLFTALFPFKNGCNDNICODDISIT 784
 DB 725 DSVTPITLRLNLTFLVGRKPLAFRLRPLAALAQRYFTASLPFEKNGGADHICODNLGIS 784
 QY 785 FSEMSLCLVVGGRPREPNVTVTNRDGEDSVRTQVTFEFLDLISYKSVSTLQNSORSW 844
 DB 785 FSPFLKSLVGVNLENAEVMWVNDGEDSYGTTITFHPAGLSYRVVAGQKQGRSL 844
 QY 845 RLACESASTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKANVTS 904
 DB 845 HLTCDSA--PVASQGTWSTSCRINHLIFRGAQITFLATFDVSPKAVLGRLLLTANVSS 902
 QY 905 ENNMPRINKTEFQLELPVKAVVAVVTVSHGVSTKYLNFITAS--ENTSRMHOYQVSNLQ 963
 DB 903 ENNTPRTSKTTFQLELPVKAVVAVVTVSSHQFTKYLNFSESEKESHVAMHYQVNNLQ 962
 QY 964 RSLPISLVLPVRLNVTIWDPRQVTFPSNLSSTCHTKERLPSHSDFLAELRKAPVNC 1023
 DB 963 RDLPSVNFVWVPELNQEAVMDEVSHPQNPSPSRCSQKIAPPASDFLAHIQKNPVLD 1022
 QY 1024 SIACVQRIQCDIPFFGIQEEFNATLKNLSFDWYIKTSHNHLIVSTAEILFNDSVFTLL 1083
 DB 1023 SIAGCLFRCDVPSFSVOEELDPTLKNLSFGVWRQLQKKSWSVVAEITFDTSVYSQL 1082
 QY 1084 PGOGAFVRSQTEKVEFPVNPPLPLVIGSSVGLLILALITALYKLGKFKKQYKQDMS 1143
 DB 1083 PGQERFMAQTITVLEKYKHNPPLVIGSSIGALLLALITALYKLVKGVFKKQYKEMME 1142
 QY 1144 E 1144
 DB 1143 E 1143

RESULT 14	
AAW65091	
ID AAW65091 standard; protein; 1163 AA.	
XX AC	
XX AAW65091;	
XX DT	
XX 28-SEP-1998 (first entry)	
XX DE Human Beta-integrin CD11c subunit protein.	
XX KW Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;	
KW type-I diabetes; atherosclerosis; multiple sclerosis; asthma;	
KW lung inflammation; acute respiratory distress syndrome; CD11c subunit;	
KW rheumatoid arthritis.	
XX OS Homo sapiens.	
XX PN US5728533-A.	
XX PD 17-MAR-1998.	
XX PF 07-JUN-1995; 95US-00485618.	
XX PR 23-DEC-1993; 93US-00173497.	
PR 05-AUG-1994; 94US-00286889.	
XX PR 21-DEC-1994; 94US-00362652.	
XX PA (ICOS-) ICOS CORP.	
PI Van Der Vieren M, Gallatin WM;	
XX WIPI; 1998-206565/18.	
XX Screening assay for modulators of integrin binding - using immobilised or	
PT labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.	
XX Example 5; Fig 1A-D; 106pp; English.	
XX This sequence represents a human beta-integrin CD11c subunit which is	
CC used to describe a method for identifying compounds that modulate the	
CC interaction of the beta-integrin alpha-d subunit with a binding partner	
CC of alpha-d which involves contacting an alpha-d polypeptide with an alpha	
CC -d binding partner, one of which is immobilised and the other of which is	
CC labelled, in the presence of a test compound, and determining if the	
CC compound affects binding between the alpha-d polypeptide and alpha-d	
CC binding partner, where the alpha-d polypeptide is alpha-d or its fragment	
CC comprising the cytoplasmic, transmembrane or extracellular domain of	
CC alpha-d. Compounds that modulate alpha-d binding could be used to treat	
CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,	
CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome	
CC and rheumatoid arthritis	
XX Sequence 1163 AA;	
SQ Query Match 58.4%; Score 3477; DB 2; Length 1163;	
Best Local Similarity 61.0%; Pred. No. 1.5e-275;	
Matches 696; Conservative 145; Mismatches 294; Indels 6; Gaps 4	
Qy 5 VLLLTALTCGFGNLDTENAMTFQENARGFGQSVVQLGSRVVVGAPQEIIVANQRGSILY 64	
Db 8 LLLFTALATSGFGLNDTEELTAFRVDSAGFGDSVVQYANSWWVVGAPOKIIAANQIGGLY 67	
Qy 65 QCDYSTCSCEPIRLQVPVEAVNMISLGLSIAATTSPQLLAGCPVTHTCSENVYKGLCF 124	
Db 68 QCQYSTACEPIGIQVPEAVNMISLGLSLASTTSPSQLLAGCPVTHTHCGRMYITGJCF 127	
Qy 125 LFSGNLRRQQPKFFEARLGCPCQEDSDIAFLDGGSGSIIPHPFRMKFEVSTVMEOKKSK 184	
Db 128 LLGPT--QLTORLPVSROECPRQEODIIVFLIDGSGSISRNFATMNFRAVISOFQRP 185	
Qy 185 TLFSLMQVSEEFRIHTFKPFQONNPNSLVKPIQLLGRTHATGIRKRVRELPNITNG 244	
Db 186 TQFSLMQPSNKFOTHTPEEFRTSNPLSLASVHQLQGFTVTATAIQNVVHRLEPHASYG 245	

XX DE Human CD11c protein sequence.

XX KW Human; macrophage infiltration inhibition; alpha d integrin;

KW Leukocyte integrin; Leu-CAM; leukointegrin; immune response;

KW inflammation; leukocyte adhesion deficiency; LAD; type I diabetes;

KW atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;

KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;

KW rheumatoid arthritis; central nervous system injury; CD11c.

XX OS Homo sapiens.

XX PN WO200029446-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-US027139.

XX PR 16-NOV-1998; 98US-00193043.

PR 08-JUL-1999; 99US-00350259.

XX PA (ICOS-) ICOS CORP.

XX PI Gallatin MW, Van Der Vieren M;

XX WIPI; 2000-387751/33.

XX Use of novel anti-alpha integrin d monoclonal antibodies to inhibit

PT macrophage infiltration and reduce inflammation at central nervous system

PT injury sites.

XX Example 5; Fig 1; 270pp; English.

CC Integrins are a class of membrane-associated molecules that participate

CC in cellular adhesion. Integrins are made up of an alpha subunit and a

CC beta subunit. One class of human integrins are restricted to expression

CC in white blood cells and have a common beta2 subunit: the leukocyte

CC integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins

CC have an important role in immune and inflammatory responses. The present

CC protein sequence is the human integrin alpha subunit CD11c. This sequence

CC was used in an alignment to identify a novel beta2 integrin alpha

CC subunit: alpha d (AA060014 and AA07359). The present sequence has

CC approximately 66% identity to the protein sequence of alpha d. The

CC Alpha d gene and protein may be useful in therapy for diseases linked to

CC aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple

CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory

CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency

CC (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the

CC inhibition of macrophage infiltration at the site of a central nervous

CC system injury. The monoclonal antibodies can also be used to detect and

CC diagnose Crohn's disease

XX Sequence 1163 AA;

Query Match 58.4%; Score 3477; DB 3; Length 1163;

Best Local Similarity 61.0%; Pred. No. 1.5e-275;

Matches 696; Conservative 145; Mismatches 294; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVLOGSRVVGAPQEIIVAAQNGSLY 64

DB 8 LLLFTALATSGFNLDTELTAFRVDSAGFGDSVVQYANVWVVGAPQKIITAAQIGGLY 67

QY 65 QCDYSTGSGCEPIRLQVPEAVNMSLGLSLAATTSPQLLACGPTVHOTCSENTYKGLCF 124

DB 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLAATTSPQLLACGPTVHHECGRMVYITGLCF 127

QY 125 LFGSNLRQOPQKFPALRGCCQEDSDIAFLIDGSGSIIPHFRMKFVSTVMQLKSK 184

DB 128 LLGPT--QTLQRLPVSRQECRQEQODIVFLIDGSGSISSRNFRATMNFRAVISQFORPS 185

QY 185 TLFLSMQYSEEPRIHFTFEKFNPNRSLVKPTITQLGRTHATGIRKVVRELFNITNG 244

DB 186 TQFSLMQFSNKFQTHFTFEERFRTSNPLSLASVHLQGLQFTYTATATQNVVHRLFHASYG 245

QY 245 ARKNAFKILVITDGEKFGDPLGYEDVPIEADREGVIRYVIGVGDAFPRSEKSRQELNTIA 304

DB 246 ARDAIKLIVITDGGKSGSDLYDVIPMDADAAGIIRYAGVGLAFQNRNSWKLNDIA 305

QY 305 SKPPRDHVQVNNFEALKTINQUREKXFAJEGTQTSSSFEHMSQEGFSAATISNGP 364

DB 306 SKPSQEHIFKVEDFDALDKIQNLKEKIFAJEGTETISSFELEMAQEGFSAVFTDGP 365

QY 365 LLSTVGSYDMAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILNRVQSILVIGAP 424

DB 366 VLGAVGSFTWSGGAPLYPPNMSPTFINNSQENVDNRDSYLGSTELALWKGVQSILVIGAP 425

QY 425 RYQHIGLVAMFRQNTQNMWESNANVKGTQIGAYFGASLCSVDVDSNGSDTLVLIGAPHYIE 484

DB 426 RYQHIGKAVIFIOVSRQWRKAEVIGTQISYFGASLCSVDVDTGSDTLVLIGAPHYIE 485

QY 485 QTRGGQSVSCPLPRGQARWQCDALYGEQOQPMGRFGAALTVLGDVNGDKLTDVAIGAP 544

DB 486 QTRGGQSVSCPLPRGWR-RWMCDAVLYGEQGHMPGRFGAALTVLGDVNGDKLTDVIGAP 544

QY 545 GEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDITWDGLVDLTV 604

DB 545 GEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDITWDGLVDLTV 604

QY 605 GAQGHVLLRSQPVLRVKAIMFENPREVARVPCNDQVVKGEAGEVRVCLHVOKSTRD 664

DB 605 GARGQVLLRTRPVLWGVSNQFIPASIPRSAFECEQVQVSEQTLVQSNICLYIDKRSKN 664

QY 665 RLREGQIQSVVYDIALDSDGRPHSAVNFETKNSRTRQTVLGTQTCTETKLKLPNCIE 724

DB 665 LLGSRDLQSSVTDLALAPGRSLSPRAIFQETKNSLSRVRVLGKAKHCENFNLLPSCVE 724

QY 725 DPVSPVILRNFSLVGCTPLSAFNGLRPVLAEDAQRLFTALPFFPKNCNDNICODDLISIT 784

DB 725 DSVIPIILRLNFTLVGKPLAFRLRLPMLAALAQRYFTASLFFPKNCAGADHICQDNLGIS 784

QY 785 FFSMSLDCLVVGGPREFNVTVTVRNDGEDSVRTQVTFFPFLDLSYRKVSTLQNRQSRSW 844

DB 785 FSPFGLKSLVGSNLELNAEVMVWVNDGEDSVGTITFSHPAGLSYRYVAEGQKQGLRSL 844

QY 845 RLACESASSTEVSGALKSTSCSINHPIPPENSEVFNITFDVDSKASLGNKLLKANVTS 904

DB 845 HLTC--CSAPVGSQGTWSTSCRIINHLIFRGAQITFLATFDVSPKAVGLDRLLLIANVSS 902

QY 905 ENNMPTNKTETFOLELPVKYAVVMVTVSHGVSTKVLNFTAS-ENTSRVMOHQYOVSNLQ 963

DB 903 ENNIPRISKITFQLELPVKYAVIIVSSHQFTKILNFSSEKESHVAMHRYQVNNLQ 962

QY 964 RSLPISLVFLVPRLNQTIVDRPQVTFSENLSSTCHTKERLPSSHSDFLAELRKAPVNC 1023

DB 963 RDLPVSIINFVVELNQEAVMMDVEVSHPPQNPSLRCSSEKIAPPASDFLAHIQKNPVLDC 1022

QY 1024 SIACVQRIQCDIPFGI:QBEFNATLKNLSPDWIKTSHNHLILVSTAEILFNDSVFTLL 1083

DB 1023 SIACGLRFRCDVPVSFSQBELDFTLKNLSFGWVRQILQKKVSVVSAEIIFTSVISQL 1082

QY 1084 PQGAFVRSOTETKVEPPEVNPPLIVGSSVGLLLALITLALYKLGPFKRYKQKDMMS 1143

DB 1083 PQGAFVRAQTITVLEKVKVHNPIPLIVGSSIGLLLALITAVLYKVGFFKRYKEMME 1142

QY 1144 E 1144

DB 1143 E 1143

Search completed: January 13, 2005, 15:12:31
Job time : 225.571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:13:36 ; Search time 190.522 Seconds
(without alignments)
2186.449 Million cell updates/sec

Title: RWHULB-A

Perfect score: 5953

Sequence: 1 MALRVLLLTALTLCGHNLD.....FKRQYKDMMSGGPGGAPQ 1153

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	5953	100.0	1153	9	US-09-350-259-3
2	5953	100.0	1153	10	US-09-902-481A-1
3	5953	100.0	1153	10	US-09-891-943-3
4	5953	100.0	1153	14	US-10-144-259-30
5	5953	100.0	1153	14	US-10-207-655-176
6	5937.5	99.7	1152	9	US-09-945-265-4
7	5865	98.5	1137	10	US-09-902-481A-6
8	5859	98.4	1137	10	US-09-902-481A-5
9	5849	98.3	1137	10	US-09-902-481A-4
10	5836	98.0	1137	10	US-09-902-481A-3
11	3500	58.8	1163	14	US-10-116-275-204
12	3500	58.8	1163	17	US-10-723-860-327
13	3477	58.4	1163	9	US-09-350-259-4

14	3477	58.4	1163	10	US-09-891-943-4	Sequence 4, Appli
15	3452	58.0	1161	9	US-09-350-259-2	Sequence 2, Appli
16	3452	58.0	1161	10	US-09-891-943-2	Sequence 2, Appli
17	3436.5	57.7	1161	9	US-09-350-259-99	Sequence 99, Appl
18	3436.5	57.7	1161	10	US-09-891-943-99	Sequence 99, Appl
19	3261	54.8	1161	9	US-09-350-259-53	Sequence 53, Appl
20	3261	54.8	1161	10	US-09-891-943-53	Sequence 53, Appl
21	3248.5	54.6	1161	9	US-09-350-259-55	Sequence 55, Appl
22	3248.5	54.6	1161	10	US-09-891-943-55	Sequence 55, Appl
23	3240	54.4	1155	9	US-09-350-259-46	Sequence 46, Appl
24	3240	54.4	1155	10	US-09-891-943-46	Sequence 46, Appl
25	3194.5	53.7	1151	9	US-09-350-259-37	Sequence 37, Appl
26	3194.5	53.7	1151	10	US-09-891-943-37	Sequence 37, Appl
27	1848	31.0	369	13	US-10-087-192-1212	Sequence 1212, Ap
28	1560	26.2	1170	9	US-09-945-265-2	Sequence 2, Appli
29	1560	26.2	1170	17	US-10-473-127-1743	Sequence 1743, Ap
30	1556.5	26.1	1145	17	US-10-872-198-130	Sequence 130, App
31	1556	26.1	1170	15	US-10-261-164-1	Sequence 1, Appli
32	1556	26.1	1170	17	US-10-473-127-1737	Sequence 1737, Ap
33	1556	26.1	1170	17	US-10-473-127-1739	Sequence 1739, Ap
34	1556	26.1	1170	17	US-10-473-127-1742	Sequence 1742, Ap
35	1552.5	26.1	1145	17	US-10-473-127-1738	Sequence 1738, Ap
36	1532.5	25.7	1223	16	US-10-408-765A-295	Sequence 295, App
37	1532.5	25.7	1223	17	US-10-473-127-1735	Sequence 1735, Ap
38	1462	24.6	1086	17	US-10-473-127-1741	Sequence 1741, Ap
39	1443.5	24.2	1065	17	US-10-473-127-1740	Sequence 1740, Ap
40	1358	22.8	1086	16	US-10-408-765A-1871	Sequence 1871, Ap
41	1358	22.8	1086	17	US-10-473-127-1735	Sequence 1735, Ap
42	1358	22.8	1086	17	US-10-473-127-1744	Sequence 1744, Ap
43	1229.5	20.7	494	9	US-09-350-259-103	Sequence 103, App
44	1229.5	20.7	494	10	US-09-891-943-103	Sequence 103, App
45	1186.5	19.9	413	9	US-09-350-259-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match 100.0%; Score 5953; DB 9; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGFGQSVVQLGSRVVVGAPOEIVAANOR 60
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Db 1141 MMSEGGPPGABPQ 1153
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; Sequence 1, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902.481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (17)..()
; OTHER INFORMATION:
US-09-902-481A-1
Query Match 100.0%; Score 5953; DB 10; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVK 120
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Db 481 HYYEOTRGQGVSVCPPLPRGORARWQCDVLYGEOQGPWRFGAALTVLGDVNGDKLTDVA 540
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Qy 1141 MMSEGGPPGAEPO 1153
Db 1141 MMSEGGPPGAEPO 1153
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RESULT 3

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; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. US20030077278A1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-891-943-3
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Query Match 100.0%; Score 5953; DB 10; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;

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Db 181 KKSKTLSLMQYSEBEFRHFTFKBPQNNPNPSLVKPIQLLGRTHATGIRKVVRELFN 240
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RESULT 4
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; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-30
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1021 VNCSTAVCORIOCDIPFPGIOEEFNATLKNLSFDWYIKTSHNHLIIVSTAEILLPNDVSF 1080
QY 1081 TLLPGCAFVSQETKVEPPEVNPPLPLIVGSSVGGILLALLITAAALYKLGFFKQYKD 1140
DB 1081 TLLPGCAFVSQETKVEPPEVNPPLPLIVGSSVGGILLALLITAAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEPQ 1153
DB 1141 MMSEGGPPGAEPQ 1153
RESULT 5
US-10-207-655-176
; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-176
Query Match 100.0%; Score 5953; DB 14; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFQGVVQLQGSRVVVGAPQEIIVAAANOR 60
DB 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFQGVVQLQGSRVVVGAPQEIIVAAANOR 60

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QY 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
DB 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFSGNLROPOKPFPEALRGCPQEDSDIAFLIDGSGIIPHFRMKFVSTVMEQL 180
DB 121 GLCFLFSGNLROPOKPFPEALRGCPQEDSDIAFLIDGSGIIPHFRMKFVSTVMEQL 180
QY 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNPSLVKPIITQLGRTHATGIRKVVRELFN 240
DB 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNPSLVKPIITQLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFALEGOTGSSSFEHMSQEGFSAIT 360
DB 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFALEGOTGSSSFEHMSQEGFSAIT 360
QY 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILNRNVQSLV 420
DB 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILNRNVQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYETRGQVSVCPPLRGORAWOCDVLYGEOQOPWGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYYETRGQVSVCPPLRGORAWOCDVLYGEOQOPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPCEEDNRGAVYLFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
DB 541 IGAPCEEDNRGAVYLFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQVPLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
DB 601 DLTVGAQGHVLLRSQVPLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDRLEQIOGVVYTDIALDSGRPHSRAVNETKNSTRROTQVGLTQTCETLKLQIP 720
DB 661 STRDRLEQIOGVVYTDIALDSGRPHSRAVNETKNSTRROTQVGLTQTCETLKLQIP 720
QY 721 NCIEDPVSPIVLRNPLSVGTPLSAFGLNRPVLAEDAQRLFTALPFPEKNCNGNDNICDD 780
DB 721 NCIEDPVSPIVLRNPLSVGTPLSAFGLNRPVLAEDAQRLFTALPFPEKNCNGNDNICDD 780
QY 781 LSITFSFMSLDCLVGGPREFNVTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNR 840
DB 781 LSITFSFMSLDCLVGGPREFNVTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNR 840
QY 841 QRSWLACESASSTEVSGALKSTCSINHPITPENSEVTFNITFDVDSKASIGNKLLKA 900
DB 841 QRSWLACESASSTEVSGALKSTCSINHPITPENSEVTFNITFDVDSKASIGNKLLKA 900
QY 901 NVTSENMPRTNKTEPQLELPVKYAVYVMTVSHGVSTKYLNFTASNTSRVMOHOVQSN 960
DB 901 NVTSENMPRTNKTEPQLELPVKYAVYVMTVSHGVSTKYLNFTASNTSRVMOHOVQSN 960
QY 961 LGQRLSPLISLFLVPVRLNQTVWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
DB 961 LGQRLSPLISLFLVPVRLNQTVWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
QY 1021 VNCSTAVCQRIQCDIPFFGIQEFNATLKGNSLFDWYIKTSHNLLIIVSTAILFNDSVF 1080
DB 1021 VNCSTAVCQRIQCDIPFFGIQEFNATLKGNSLFDWYIKTSHNLLIIVSTAILFNDSVF 1080
QY 1081 TLLPGQCAFVRSQTEKVPFVNPPLPLIVGSSVGGILLALLITAAALKYKGFKKQYKD 1140
DB 1081 TLLPGQCAFVRSQTEKVPFVNPPLPLIVGSSVGGILLALLITAAALKYKGFKKQYKD 1140
QY 1141 MMSEGPPGAEPQ 1153
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DB 1141 MMSEGPPGAEPQ 1153
RESULT 6
US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4
Query Match 99.7%; Score 5937.5; DB 9; Length 1152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1151; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAANQR 60
DB 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAANQR 60
QY 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
DB 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFSGNLROPOKPFPEALRGCPQEDSDIAFLIDGSGIIPHFRMKFVSTVMEQL 180
DB 121 GLCFLFSGNLROPOKPFPEALRGCPQEDSDIAFLIDGSGIIPHFRMKFVSTVMEQL 180
QY 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNPSLVKPIITQLGRTHATGIRKVVRELFN 240
DB 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNPSLVKPIITQLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFALEGOTGSSSFEHMSQEGFSAIT 360
DB 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFALEGOTGSSSFEHMSQEGFSAIT 360
QY 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILNRNVQSLV 420
DB 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILNRNVQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYETRGQVSVCPPLRGORAWOCDVLYGEOQOPWGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYYETRGQVSVCPPLRGORAWOCDVLYGEOQOPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPCEEDNRGAVYLFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
DB 540 IGAPCEEDNRGAVYLFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
QY 601 DLTVGAQGHVLLRSQVPLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
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Db 600 DLTVGAQGHVLLRSQVLRVKALMEFNPREVARNVFECDNDQVVGKEAGEVRVCLHVQK 659
QY 661 STRDLREGIOQSVVTVYDLALDSGRPHSRVAFNETKNSRRQTVGLTQTCETLKLQLP 720
Db 660 STRDLREGIOQSVVTVYDLALDSGRPHSRVAFNETKNSRRQTVGLTQTCETLKLQLP 719
QY 721 NCIEDPVSPIVLRNLSFVLGTPLSAFGNLPLVLAEDAQRLLFTALFFPEKNCNDNIQQDD 780
Db 720 NCIEDPVSPIVLRNLSFVLGTPLSAFGNLPLVLAEDAQRLLFTALFFPEKNCNDNIQQDD 779
QY 781 LSITFSFMSDCLVVGPRFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNR 840
Db 780 LSITFSFMSDCLVVGPRFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNR 839
QY 841 QRSWRLACESASSTVSGALKSTSCSINHPIPFENSEVFNITFDVDSKASLGNKLLIKA 900
Db 840 QRSWRLACESASSTVSGALKSTSCSINHPIPFENSEVFNITFDVDSKASLGNKLLIKA 899
QY 901 NVTSNNMPTNKTEFQLELPVKIYAVMVVTVSHGVSTKYNLFTASENTSRVMQHOVQSN 960
Db 900 NVTSNNMPTNKTEFQLELPVKIYAVMVVTVSHGVSTKYNLFTASENTSRVMQHOVQSN 959
QY 961 LGORSLSPIVLRNLSFVLGTPLSAFGNLPLVLAEDAQRLLFTALFFPEKNCNDNIQQDD 1020
Db 960 LGORSLSPIVLRNLSFVLGTPLSAFGNLPLVLAEDAQRLLFTALFFPEKNCNDNIQQDD 1019
QY 1021 VNCISIAVCQRIQCDIPFFGQIEEFNATLKNLSFDWYIKTSHNHLIIVSTAELFNDSVF 1080
Db 1020 VNCISIAVCQRIQCDIPFFGQIEEFNATLKNLSFDWYIKTSHNHLIIVSTAELFNDSVF 1079
QY 1081 TLLPGQCAFVRSQTEKVPFFVNPPLIIVGSSVGLLALLIITAALYKLGFFKRYQKD 1140
Db 1080 TLLPGQCAFVRSQTEKVPFFVNPPLIIVGSSVGLLALLIITAALYKLGFFKRYQKD 1139
QY 1141 MMSEGGPPGAEPQ 1153
Db 1140 MMSEGGPPGAEPQ 1152

RESULT 7
US-09-902-481A-6
; Sequence 6, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimadzu, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; FILE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-6

Query Match 98.5%; Score 5865; DB 10; Length 1137;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1132; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 17 FNLDTENAMTFOENARGQSVQVQOGSRVVVGAPOEIVAAOQSGSLYQCDYSTGSCPEI 76
Db 1 FNLDTENAMTFOENARGQSVQVQOGSRVVVGAPOEIVAAOQSGSLYQCDYSTGSCPEI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHTCSENTYVKGCLFLGSLNRQQPQK 136

US-09-902-481A-5
; Sequence 5, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-5
Query Match 98.4%; Score 5859; DB 10; Length 1137;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1128; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
QY 17 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIVAANQSGSLYQCDYSTGSCBPI 76
DB 1 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIVAANQSGSLYQCDYSTGSCBPI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHQTCSNTYVKGCLFGLFNSLRQQPK 136
DB 61 RLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHQTCSNTYVKGCLFGLFNSLRQQPK 120
QY 137 FPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMEQLKSKTFLSLMOYSBEF 196
DB 121 FPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMEQLKSKTFLSLMOYSBEF 180
QY 197 RIHFTFKFQNNPNSRLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVI 256
DB 181 RIHFTFKFQNNPNSRLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVI 240
QY 257 TDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDRHVQVN 316
DB 241 TDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDRHVQVN 300
QY 317 NPEALKTONQUREKFAIEGTQTSSSSFEHMSQEGFSAAITSGNPLLSVTGSDYDWAG 376
DB 301 NPEALKTONQUREKFAIEGTQTSSSSFEHMSQEGFSAAITSGNPLLSVTGSDYDWAG 360
QY 377 GVFLYTSKEKSTFINNTRVDSMDNAYLGAAIILRNVRQSLVLGAPRYQHIGLVAMFR 436
DB 361 GVFLYTSKEKSTFINNTRVDSMDNAYLGAAIILRNVRQSLVLGAPRYQHIGLVAMFR 420
QY 437 QNTGWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLVIGAPHYYEQTGRGGVSVCPL 496
DB 421 QNTGWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLVIGAPHYYEQTGRGGVSVCPL 480
QY 497 PRGQARWQCDVAVLGEQGPWGRFGAALTVDGVNKGDKLTDVAICAPGEEDNRGAVYLF 556
DB 481 PRGQARWQCDVAVLGEQGPWGRFGAALTVDGVNKGDKLTDVAICAPGEEDNRGAVYLF 540
QY 557 HGTSGSGISPSHSQRIAGSKLSPLQYFGOSLGGQDLTMDGLVDLTVCAGQGHVLLRSQ 616
DB 541 HGTSGSGISPSHSQRIAGSKLSPLQYFGOSLGGQDLTMDGLVDLTVCAGQGHVLLRSQ 600
QY 617 PVLVRKAIIMEFNPREVARNVFCNDQVVKGEAGEVRVCLHVQKSTRDLREGQIQSVVT 676
DB 601 PVLVRKAIIMEFNPREVARNVFCNDQVVKGEAGEVRVCLHVQKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRVFNFTKSTRQTQVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 736

DB 661 YDLALDSGRPHSRVFNFTKSTRQTQVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFGNLRPLVLAEDAQRLLFTALFPPEKKNCGNDNI CODDLSITFSFMSLDCLVVG 796
DB 721 SLVGTPLSAFGNLRPLVLAEDAQRLLFTALFPPEKKNCGNDNI CODDLSITFSFMSLDCLVVG 780
QY 797 GPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRQSRWRLACESASSTEV 856
DB 781 GPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRQSRWRLACESASSTEV 840
QY 857 SGALKSTSCSINHPIFPENSEVTENITFDVDSKASLGNKLLKANVTSENNMPTNKTEF 916
DB 841 SGALKSTSCSINHPIFPENSEVTENITFDVDSKASLGNKLLKANVTSENNMPTNKTEF 900
QY 917 QLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQYQVSNLQGSRLPSLVFLVPV 976
DB 901 QLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQYQVSNLQGSRLPSLVFLVPV 960
QY 977 RLNQTVIWDPRQVTFSENLSTCHTKERLPHSDPLAELRKAPVNVNCISIAVCQRIQCDDIP 1036
DB 961 RLNQTVIWDPRQVTFSENLSTCHTKERLPHSDPLAELRKAPVNVNCISIAVCQRIQCDDIP 1020
QY 1037 FPGIOEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDSVFTLLPGQGAFAVRSOTET 1096
DB 1021 FPGIOEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDSVFTLLPGQGAFAVRSOTET 1080
QY 1097 KVEPPEVENPPLIVGVSSVGGLLIALLIATAALYKLGFFKQYKDMMSGGPPGABPQ 1153
DB 1081 KVEPPEVENPPLIVGVSSVGGLLIALLIATAALYKLGFFKQYKDMMSGGPPGABPQ 1137
RESULT 9
US-09-902-481A-4
; Sequence 4, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-4
Query Match 98.3%; Score 5849; DB 10; Length 1137;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1127; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 17 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIVAANQSGSLYQCDYSTGSCBPI 76
DB 1 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIVAANQSGSLYQCDYSTGSCBPI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHQTCSNTYVKGCLFGLFNSLRQQPK 136
DB 61 RLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHQTCSNTYVKGCLFGLFNSLRQQPK 120
QY 137 FPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMEQLKSKTFLSLMOYSBEF 196
DB 121 FPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMEQLKSKTFLSLMOYSBEF 180

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QY 197 RIHFTKEFQNNPNRSLVKPTTOLLGRTHHTATGRKVVRELFNITNGARKNAFKILVVI 256
Db 181 RIHFTKEFQNNPNRSLVKPTTOLLGRTHHTATGRKVVRELFNITNGARKNAFKILFLL 240
QY 257 TDGEKFGDPLGYEDVPEADREGVIRYVIGDAPRSEKSRQELNTIASKPPDRDHVFOVN 316
Db 241 TDGEKFGDPLGYEDVPEADREGVIRYVIGDAPRSEKSRQELNTIASKPPDRDHVFOVN 300
QY 317 NFEALKTIONLREKXFAIEGTQTGSSSSFEHMSQEGFSAAITNGPLLSITVGSYDQWAG 376
Db 301 NFEALKTIONLREKXFAIEGTQTGSSSSFEHMSQEGFSAAITNGPLLSITVGSYDQWAG 360
QY 377 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLVIGAPRYOHIGLVAMFR 436
Db 361 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLVIGAPRYOHIGLVAMFR 420
QY 437 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYEQTRGGQVSVCP 496
Db 421 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYEQTRGGQVSVCP 480
QY 497 PRGQARWQCDVAVLYGEOQPGWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 556
Db 481 PRGQARWQCDVAVLYGEOQPGWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 540
QY 557 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 616
Db 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 600
QY 617 PVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 676
Db 601 PVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 736
Db 661 YDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFNGNLRPVLAEADAQRLLFTALFFPEKNCNDNI CODDLSITFSFMSLDCLVVG 796
Db 721 SLVGTPLSAFNGNLRPVLAEADAQRLLFTALFFPEKNCNDNI CODDLSITFSFMSLDCLVVG 780
QY 797 GPREFNVTVRNDGEDSVRTQVTFPPDLDSYRKVSTLQNRQSRWRLACESASSTEV 856
Db 781 GPREFNVTVRNDGEDSVRTQVTFPPDLDSYRKVSTLQNRQSRWRLACESASSTEV 840
QY 857 SGALKSTCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRINKTEF 916
Db 841 SGALKSTCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRINKTEF 900
QY 917 QLELPVKAVYVMVTSHGVS TKYLNFTASENTRVMOHQYQVSNIGQSRSLPISLVFLVPV 976
Db 901 QLELPVKAVYVMVTSHGVS TKYLNFTASENTRVMOHQYQVSNIGQSRSLPISLVFLVPV 960
QY 977 RLNQTVIWDROPVTFSENLSSTCHTKERLPHSDFLAELRKAPVVCNSIAVCORIQCDIP 1036
Db 961 RLNQTVIWDROPVTFSENLSSTCHTKERLPHSDFLAELRKAPVVCNSIAVCORIQCDIP 1020
QY 1037 PFGIQEEFNATLKGNSLFDWIKTSHNHLIVSTAEILFNDSVFTLLPQCGAFVRSQTE 1096
Db 1021 PFGIQEEFNATLKGNSLFDWIKTSHNHLIVSTAEILFNDSVFTLLPQCGAFVRSQTE 1080
QY 1097 KVEPPEVNPLPIVGVSSVGLLILALITAAALYKLGFFKQYKQKDMSEGGPPGAPQ 1153
Db 1081 KVEPPEVNPLPIVGVSSVGLLILALITAAALYKLGFFKQYKQKDMSEGGPPGAPQ 1137
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RESULT 10

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US-09-902-481A-3
; Sequence 3, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
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; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-3
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Query Match 98.0%; Score 5836; DB 10; Length 1137;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1123; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
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QY 17 ENLDTENAMTFOENARGFGOSVVOLOQSRVVVGAPQEIIVAAANQSGSLYQCDYSTGSCPEI 76
Db 1 ENLDTENAMTFOENARGFGOSVVOLOQSRVVVGAPQEIIVAAANQSGSLYQCDYSTGSCPEI 60
QY 77 RLQVPVEAVNMSLGLSLAAATSPPLLACGPTVHTQTCSENTYVVKGLCFLFGSNLRQPOK 136
Db 61 RLQVPVEAVNMSLGLSLAAATSPPLLACGPTVHTQTCSENTYVVKGLCFLFGSNLRQPOK 120
QY 137 PPEALRGCPQSDSDIAFLIDGSGSIIIPDFFRMKEFVSTVMEQKKSKTLFSLMOYSEEP 196
Db 121 PPEALRGCPQSDSDIAFLIDGSGSIIIPDFFRMKEFVSTVMEQKKSKTLFSLMOYSEEP 180
QY 197 RIHTEKEFQNNPNRSLVKPTTOLLGRTHHTATGRKVVRELFNITNGARKNAFKILVVI 256
Db 181 RIHTEKEFQNNPNRSLVKPTTOLLGRTHHTATGRKVVRELFNITNGARKNAFKILFLL 240
QY 257 TDGEKFGDPLGYEDVPEADREGVIRYVIGDAPRSEKSRQELNTIASKPPDRDHVFOVN 316
Db 241 TDGEKFGDPLGYEDVPEADREGVIRYVIGDAPRSEKSRQELNTIASKPPDRDHVFOVN 300
QY 317 NFEALKTIONLREKXFAIEGTQTGSSSSFEHMSQEGFSAAITNGPLLSITVGSYDQWAG 376
Db 301 NFEALKTIONLREKXFAIEGTQTGSSSSFEHMSQEGFSAAITNGPLLSITVGSYDQWAG 360
QY 377 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLVIGAPRYOHIGLVAMFR 436
Db 361 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLVIGAPRYOHIGLVAMFR 420
QY 437 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYEQTRGGQVSVCP 496
Db 421 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYEQTRGGQVSVCP 480
QY 497 PRGQARWQCDVAVLYGEOQPGWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 556
Db 481 PRGQARWQCDVAVLYGEOQPGWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 540
QY 557 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 616
Db 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 600
QY 617 PVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 676
Db 601 PVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 736
Db 661 YDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFNGNLRPVLAEADAQRLLFTALFFPEKNCNDNI CODDLSITFSFMSLDCLVVG 796
Db 721 SLVGTPLSAFNGNLRPVLAEADAQRLLFTALFFPEKNCNDNI CODDLSITFSFMSLDCLVVG 780
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QY 797 GPRENVTVVRNDCGSDSYRTQVTFPPFDLSYRKVSTLQNRORSWRLACESASSTEV 856
DB 781 GPRENVTVVRNDCGSDSYRTQVTFPPFDLSYRKVSTLQNRORSWRLACESASSTEV 840
QY 857 SGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTSENNMPTNKTEP 916
DB 841 SGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTSENNMPTNKTEP 900
QY 917 QLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMQHQYQVSNLQORSLSPLSVFLVPV 976
DB 901 QLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMQHQYQVSNLQORSLSPLSVFLVPV 960
QY 977 RLNQTVIWRDPQVTSSENLSSCTCHTKERLPSHDSFLAELRKAPVNVNCISIAVCORIQCDDIP 1036
DB 961 RLNQTVIWRDPQVTSSENLSSCTCHTKERLPSHDSFLAELRKAPVNVNCISIAVCORIQCDDIP 1020
QY 1037 PFGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDVSFTLLPQOGAFVRSQTEP 1096
DB 1021 PFGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDVSFTLLPQOGAFVRSQTEP 1080
QY 1097 KVEPPEVFNPLPLIVGSSVGGILLALITAAALYKLGFFKQYKQVNMWSEGGPPGAEPPQ 1153
DB 1081 KVEPPEVFNPLPLIVGSSVGGILLALITAAALYKLGFFKQYKQVNMWSEGGPPGAEPPQ 1137

RESULT 11
US-10-116-275-204
; Sequence 204, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-204

Query Match 58.8%; Score 3500; DB 14; Length 1163;
Best Local Similarity 61.3%; Pred. No. 6.8e-280;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHEFNLDNTENMTFOENARGFGSVQVLOGSRVVGAPQEIIVANQORSIJ 64
DB 8 LLLFTALATSLGFLNLDTELTAFRDYAGFGDSVQYANVWVGAPQKITAANQTGLY 67
QY 65 QCDYGTGSCPTRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVKGLCF 124
DB 68 QCGYGTGACEPICLQVPEAVNMSLGLSLASTTSQQLACGPTVHCEGRNMYTGLCF 127
QY 125 LFGSNLRQOPKFPBALRGCPQEDSDIAPLIDGSGSIIPHPDPRMKEFVSTVMEQLKXSK 184
DB 128 LLGPT--QUTRLPVSRQBCPQEQDIFVLIDGSGSISRNPNATMNFVRAVISQFQRP 185
QY 185 TLPSLMQYSEERIHFTKEPQNPNRSLVXPITQLGRHTATGIRKVVRELNIYNG 244
DB 186 TOFSLMQFSNKTQTHTEEPFRTPNPLSLASVHQLQGYTATATQVNVHRLPHASVG 245
QY 245 ARKNAPKILWITDGEKFDPLGYEDVPEADREGVIRVVGDAFRSEKSRQELNITIA 304
DB 246 ARDATKILIVITDGKSGDSLVDKDVIPMADAAGIIRYVIGLAFQNRNSWKLNDIA 305
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QY 305 SKPRDRHVQVNNPEALKTIONREKXPALEGTOQTSSSSFEHMSQEGSAAITSNGP 364
DB 306 SKPSQEHIFKVEDFDALKDIONLKEKIFAIEGTETTTSSSSFELEMAQEGSAVPTDGP 365
QY 365 LLSTVGSVDWAGGVPLVTSKESKTFINMTRVDSNDWDAYLVAAAIILRNVRQSVLVLGAP 424
DB 366 VLGAVGSTWGGAFPLPPNMSPTFINNSQENVDNRDSILGYSTELALWKGVQSVLVLGAP 425
QY 425 RYOHIGLVAMFRQNTGMWESNANYKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE 484
DB 426 RYQHTGRAVITQVSRQWRMKAETVGTQIGSYFGASLCSVDVDTGSDTLVLIGAPHYYE 485
QY 485 QTRGGQSVVCLPRQQRARWOCDAVLGEGQQQWGRFGAALTVLGDNVGDKLTDLVAIGAP 544
DB 486 QTRGGQSVVCLPRGWR--RWCMDAVLYGEGQHPGRFGAALTVLGDNVGDKLTDLVIGAP 544
QY 545 GEENRGAVLYFHTGSSGSI SPSSHQSORTAGSKLSPQLQYFGQSLSGGGDLTMDGLVDLTV 604
DB 545 GEENRGAVLYFHTGSSGSI SPSSHQSORTAGSKLSPQLQYFGQSLSGGGDLTMDGLVDLTV 604
QY 605 GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECDQVVRKGEAGEVRVCLHVKQSTRD 664
DB 605 GARGOVLLLRTPVLRVGVSMQFIPAEIPRSAFECEQVWSEQTLVQSNICLIYDKRSKN 664
QY 724 RLREGQIQSVTYDLALDSGRPHSRVAFNETKSTRQTVGLGLTQTCETLKLQPLNCIE 724
DB 665 LLGSRDLQSSVTLDLALDPGRSLSPRATFQETKNSLSRVRVLGKAHCENFLLPSCVB 724
QY 725 DPVSPVILRLNFSLVGTPLSAFNLRPVLAEDADQLFTALPFEKNCNDNICODDLST 784
DB 725 DSVTPITLRLNFTLVGKPLLAFLRMLPMLAALQRYFTASLPFEKNCADHICQDNILGIS 784
QY 785 FSPMSLDCLVGGPREFNVTYVRNDGSDSYRTQVTFPPFDLSYRKVSTLQNRORSW 844
DB 785 FSPFGLKSLVGSNLENAEVMWVNDGSDSYRTQVTFPPFDLSYRKVSTLQNRORSW 844
QY 845 RLACESASTSEVGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVT 904
DB 845 HLTCDSPVPG--SQGTWSTSCRIINHLIPRGAQITFLATFDVSPKAVLGDRLLLTANVSS 902
QY 905 ENNMPTNKTBFQLELPVKYAVVMVTVSHGVSTKYLNFTAS--ENTSRVMOHQYVSNLQ 963
DB 903 ENNTPTSKTTFQLELPVKYAVVMVTVSHGVSTKYLNFTAS--ENTSRVMOHQYVSNLQ 962
QY 964 RSLPISLVFLVPLRNLQTVIWRDPQVTSSENLSSCTCHTKERLPSHDSFLAELRKAPVNVNC 1023
DB 963 RDLPVSVINFWVPVELNQEAVMWVESHVPQNSPRLCSSEKIAPPASDFLAHIQKNPVLDC 1022
QY 1024 SIACVQRIQCDDIPFPGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDVSFTLL 1083
DB 1023 SIAGCLRFRCDDVPSPVQOEELDTLKGNSLFGWVRQILQKKVSVSVSAEITFDTSVYSQL 1082
QY 1084 PQOGAFVRSQTEKVEPEVFNPLPLIVGSSVGGILLALITAAALYKLGFFKQYKQVNMW 1143
DB 1083 PQOGAFVRSQTEKVEPEVFNPLPLIVGSSVGGILLALITAAALYKLGFFKQYKQVNMW 1142
QY 1144 E 1144
DB 1143 E 1143

RESULT 12
US-10-723-860-327
; Sequence 327, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
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; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 327
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-327

Query Match      58.8%; Score 3500; DB 17; Length 1163;
Best Local Similarity 61.3%; Pred. No. 6.8e-280;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHFNLDTENAMTFQENARGFQSVVQLQSGRVVVGAPQEIIVAAHQSGSLY 64
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Db 8 LLLFTALATSLGFLNLDTEELTAFRVDSAGFQSVVQYANVWVVGAPQKITAAQTGGLY 67

QY 65 QCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLIACGPTVHQTCSNTYVKGCLCF 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 QCGYSTGACCEPIGLQVPPPEAVNMSLGLSLASTTSPQLLACGPTVHHECGRNWYLTGLCF 127

QY 125 LFGSNLRQOPQKFPPEALRCCPEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSK 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 128 LLGPT--QLTQRLPVSRQECPRQEQDIVFLIDGSGSISSRNPFATMNFVRAVISQFQPS 185

QY 185 TFLSLMOWSEEFRIHFTPFKEFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNG 244
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 TQFSLMQFSNKFQTHFTFEERPRTSNPLSLASVHQLQGGFTTATAIQNVVHRLPHASVG 245

QY 245 ARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIA 304
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 246 ARRDATKILVITDGKKEGSDLDYKDVIPMDAAGIIRYAGVGLAFQNRNSWKELNDIA 305

QY 305 SKPPRDHFQVNNFALKTIQNLREKKAIPAIGTQSGSSSEHEHMSQEGFSAALTSGKP 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 306 SKPSQEHIPKVBDFDALKDQNLREKKAIPAIBGTETSSSSFELEMAQEGFSAVFTPDGP 365

QY 365 LLSTVGSVDWAGGVFLYTSKSKSTFTNTRVDSMDNDAVLYAAAIILNRVQSLVIGAP 424
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 366 VLGVGSGFTWAGGAFLYPPNMGPTFINNSQENVMDRDSYLGYSTELALWKGVSILVIGAP 425

QY 425 RYOHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSDVDSDNGSTDVLVIGAPHYFE 484
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 426 RYOHGTGKAVIFTQVSRQWRMKAEVGTQIGSYFGASLCSDVDVTDGSTDVLVIGAPHYFE 485

QY 485 QTRGGQVSVCPILPRGORARWQCDVLYGEOGQWGRFGAALTIVLGDVNGDKLTDVIGAP 544
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 486 QTRGGQVSVCPILPRGWR--RWWCDVLYGEOGHPGRFGAALTIVLGDVNGDKLTDVIGAP 544

QY 545 GEDNRGAVYLPHTGSGSISPSHSORISAGSKLSPRLQVFGQSLGGQDLTMDGLVDLTV 604
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 545 GEEENRGAVYLPHTGSGSISPSHSORISAGSKLSPRLQVFGQALSGQDLTQDGLVDLAV 604

QY 605 GAQGHVLLRSQPLVLRKAIEMFNPREVARNVFECDQVVKGEAGEVRVCLVHVKQSTRD 664
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 605 GARGQVLLRLTRPVLWVGVMQFIPAEIIPRSFAFECREQVVSQTLVQSNICLYIDKRSKN 664

QY 665 RLREGQIQSVTYDIALDGRPHSAVNETKNSRTQTVLGLTQTCETLKLQIPLNCIE 724
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 665 LLGSRDLOSSVTLDALDPGRSLPRATFOETKNSRLSRVRLGLKAHCENFNLLPSQVE 724

QY 725 DPVSVTLRLNPLSVGTPLSAFNGRLPVLAEDAORLFTALFPFEKNCNGNDNICQDDLSIT 784
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 725 DSVTITLRLNPLSVGTPLSAFNGRLPVLAEDAORLFTALFPFEKNCNGADHICQDNIGIS 784

QY 785 F5FM5LDCVLVGGPREFNVTVTRNDGEDSYRTQVTFPPFDLSYKXSTLQNRQSRSW 844
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 785 F5FPGKLSLLVGNLELNAEVNMDGEDSYGTTITFSGHAGLSYRYVAEGQKQQLRSL 844

QY 845 RLACESASSTVSGALKSTSCSINHPIIPENSEVTFNITFDVDSKASLGNKLLKANVTS 904
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Db 246 ARDAIKLIVITDGGKESDLDYKDVIPMAAAGIIRYAIGVGLAFQNRNSWKELNDIA 305
Qy 305 SKPPRDHVQVNNFALKTIQNLQREKXFAIEGTOTGSSSSPEHEMSQEGFAAITSNGP 364
Db 306 SKPSQEHIFKVEDFDALDKIQNLQREKIFAIEGTETISSSSFELEMAQEGFAVTPDGP 365
Qy 365 LLSTVGSVDWAGGVFLYTSKEKSTFINNTRVDSNMNDAYLGAAAAIILNRNQSIVLGAP 424
Db 366 VLGAAGSFTWGGAFLLPPNMSPTFINMSQENVDNRDSYLGYSTELALWKGVQSVLVLGAP 425
Qy 425 RYQHGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLVIGAPHYYE 484
Db 426 RYQHGLKAVIFIQVSRQWRMKAIEVGTQIGSYFGASLCSVDVDTGSDTDLVIGAPHYYE 485
Qy 485 QTRGGQVSVCPPLRGQARWOCDAVLYGEGQGPWGRFGAALTIVLGDVNGDKLTDVAIGAP 544
Db 486 QTRGGQVSVCPPLRGWR-RWMCDAVLYGEGQHPWGRFGAALTIVLGDVNGDKLTDVVIGAP 544
Qy 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLGGQDLTMDGLVLT 604
Db 545 GSEENRGAVYLFHGVLPSPISPSHSQRIAGSKLSRLQYFGQALSGGQDLTQDGLVDLAV 604
Qy 605 GAQGHVLLRSQPLVRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVQKSTRD 664
Db 605 GARGOVLLLRTPVLVWGVSMQFIPAEIPRSAFECEQVVSQTLVQSNICLYIDKRSKN 664
Qy 665 RLREGQIOSVVTYDIALDSGRPHSAVFNETKNSRTRQTVLGLTQCTETLKLQLPNCIE 724
Db 665 LLGSRDLQSSVTLDALAPGRLSPRAIPOETKNRSLSRVRLGLKAHCENFNLLPSCVE 724
Qy 725 DPVSPVILRLNFSLVGTPLSAFNLRLVLAEDAORLFTALPFPEKNCNDNICODDLSIT 784
Db 725 DSVIPIILRLNFTLVGKPLLAFLNRLPMLAALQRYFTASLPFEKNCAGADHICQDNLGIS 784
Qy 785 FEFMSLDCLVYCGPREFNVTVTRDGEDSYQTQVTFPPDLDSYRKUSTLQNRQSRW 844
Db 785 FSFPGKLSLLVGSNLELNAEVMVMNDGEDSYGTTTTFSPAGLSYRYAEGQKQGLRSL 844
Qy 845 RLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANVTS 904
Db 845 HLTC--CSAPVCSQGTWSTSCINHLIFRGGAQITFLATFDVSPKAVGLDRLLLTANVSS 902
Qy 905 ENNMPTNKTQELPVLKYAVYVMTSHGVSTKYLNFAS-ENTSRVQHQQYVSNLQ 963
Db 903 ENNIPRTKTIQELPVLKYAVYVVSSEHQTKYLNFSSEKESHVAMHRYQVNNLQ 962
Qy 964 RSLPISLVPLVRLNQTWIDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKPVNC 1023
Db 963 RDLPSVSNFVWVPELNQEAVMMDVEVSHPPQNPSPRCSEKIAAPPASDFLAHTQKNPVLD 1022
Qy 1024 SIACVQRIQCDIPFFGQIEFNATLKNLSFDWYIKTSHNHLIIVSTAELPNDVSFTLL 1083
Db 1023 SIAGCLRFCDVPSVQBELDFTLKNLSFGWVQILQKVVSVSVABEIIIDTSVSYQL 1082
Qy 1084 PQGAFVRSQTKVEPVPNPLPLIVGSSVGGLLLALITAAALYKLGFFKRYQKMDMS 1143
Db 1083 PQGEAFMRAQTITVLEKYVKNPIPLIVGSSIGGLLALITAVLYKVYGFPRQYKENME 1142
Qy 1144 E 1144
Db 1143 E 1143
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RESULT 14

US-09-891-943-4

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; Sequence 4, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
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; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-891-943-4
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Query Match 58.4%; Score 3477; DB 10; Length 1163;

Best Local Similarity 61.0%; Pred. No. 5.5e-278;

Matches 696; Conservative 145; Mismatches 294; Indels 6; Gaps 4;

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Db 8 LLLFTALATSLGFNLDTEELTAFRVDVSAGFGDSVVQYANSMWVVGAPQKIIAANOIGGLY 67
Qy 65 QCDYSTGSCPTRLQVPVEAVNMSLGLAATTPPQLLACGPTVHOTCSENTYYVKGCLF 124
Db 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLASTTSPQLLACGPTVHHECGRNMYLTGLCF 127
Qy 125 LFGSNLRQOPKFPBALRGCPQEDSIAPLIDGSGSIIPHDFRRMKFVSTVMEQKKSK 184
Db 128 LLGPT--QLTQRLPVSROCEQEDIVFLIDGSGSISSRNFMFVRAVISQFRPS 185
Qy 185 TLFSLMQYSEFRTHFTPEKQNNPRSLVKPITQLLGRTHATGIRKVVRELNIWNG 244
Db 186 TQFSLMQFSNKFQTHFTFEERFRTSNPLSLASVHQLQGFYTTATAIQNVHRLPHASYG 245
Qy 245 ARKNAFKILVITDCEKFGDPLGVEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIA 304
Db 246 ARDAIKLIVITDGGKESDLDYKDVIPMAAAGIIRYAIGVGLAFQNRNSWKELNDIA 305
Qy 305 SKPPRDHVQVNNFALKTIQNLQREKXFAIEGTOTGSSSSPEHEMSQEGFAAITSNGP 364
Db 306 SKPSQEHIFKVEDFDALDKIQNLQREKIFAIEGTETISSSSFELEMAQEGFAVTPDGP 365
Qy 365 LLSTVGSVDWAGGVFLYTSKEKSTFINNTRVDSNMNDAYLGAAAAIILNRNQSIVLGAP 424
Db 366 VLGAAGSFTWGGAFLLPPNMSPTFINMSQENVDNRDSYLGYSTELALWKGVQSVLVLGAP 425
Qy 425 RYQHGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLVIGAPHYYE 484
Db 426 RYQHGLKAVIFIQVSRQWRMKAIEVGTQIGSYFGASLCSVDVDTGSDTDLVIGAPHYYE 485
Qy 485 QTRGGQVSVCPPLRGQARWOCDAVLYGEGQGPWGRFGAALTIVLGDVNGDKLTDVAIGAP 544
Db 486 QTRGGQVSVCPPLRGWR-RWMCDAVLYGEGQHPWGRFGAALTIVLGDVNGDKLTDVVIGAP 544
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Db 545 GSEENRGAVYLFHGVLPSPISPSHSQRIAGSKLSRLQYFGQALSGGQDLTQDGLVDLAV 604
Qy 605 GAQGHVLLRSQPLVRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVQKSTRD 664
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Qy 665 RLREGQIOSVVTYDIALDSGRPHSAVFNETKNSRTRQTVLGLTQCTETLKLQLPNCIE 724
Db 665 LLGSRDLQSSVTLDALAPGRLSPRAIPOETKNRSLSRVRLGLKAHCENFNLLPSCVE 724
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 55.4108 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWHULB-A
Perfect score: 5953
Sequence: 1 MALRVLLLTALTLCHGFNLD.....FKRQYKDMSEGGPGAPQ 1153

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5953	100.0	1153	1 US-08-173-497-3	Sequence 3, Appli
2	5953	100.0	1153	1 US-08-286-889-3	Sequence 3, Appli
3	5953	100.0	1153	1 US-08-485-618-3	Sequence 3, Appli
4	5953	100.0	1153	1 US-08-362-652-3	Sequence 3, Appli
5	5953	100.0	1153	2 US-08-605-672-3	Sequence 3, Appli
6	5953	100.0	1153	2 US-08-482-293A-3	Sequence 3, Appli
7	5953	100.0	1153	2 US-08-943-363-3	Sequence 3, Appli
8	5953	100.0	1153	3 US-09-193-043-3	Sequence 3, Appli
9	5953	100.0	1153	4 US-09-688-307A-3	Sequence 3, Appli
10	5953	100.0	1153	4 US-09-350-259-3	Sequence 3, Appli
11	5922.5	99.5	1152	2 US-08-476-062A-43	Sequence 43, Appl
12	5922.5	99.5	1152	5 PCT-US96-01314-43	Patent No. 5424399
13	5922.5	99.5	1152	6 5424399-2	Sequence 44, Appl
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23	3477	58.4	1163	3 US-09-193-043-4	Sequence 4, Appli
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36	3436.5	57.7	1161	1 US-08-485-618-99	Sequence 99, Appl
37	3436.5	57.7	1161	2 US-08-605-672-99	Sequence 99, Appl
38	3436.5	57.7	1161	2 US-08-482-293A-99	Sequence 99, Appl
39	3436.5	57.7	1161	2 US-08-943-363-99	Sequence 99, Appl
40	3436.5	57.7	1161	3 US-09-193-043-99	Sequence 99, Appl
41	3436.5	57.7	1161	4 US-09-688-307A-99	Sequence 99, Appl
42	3436.5	57.7	1161	4 US-09-350-259-99	Sequence 99, Appl
43	3261	54.8	1161	1 US-08-485-618-53	Sequence 53, Appl
44	3261	54.8	1161	1 US-08-362-652-53	Sequence 53, Appl
45	3261	54.8	1161	2 US-08-605-672-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-173-497-3
; Sequence 3, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-173-497-3

Query Match 100.0%; Score 5953; DB 1; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARFGQSVVQLGSGRVVVGAPQEIIVANOR 60
DB 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARFGQSVVQLGSGRVVVGAPQEIIVANOR 60

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DB 181 KSKTILFSLMOYSEEPRIHFTFKFQNNPNPSLVKPIITOLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKGDPLGYEDVPIEADREGVIRVYVGVGDAPFSEKSRBEL 300
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QY 1141 MMSEGGPPGABPQ 1153
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RESULT 2
US-08-286-889-3
; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/286,889
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-3
Query Match 100.0%; Score 5953; DB 1; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-3

Query Match 100.0%; Score 5953; DB 1; Length 1153;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGFQSVVQLQGSRVVVGAPQEIIVAANOR 60
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Db 61 GSLYQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATTSPQLLAGCPTVHQTCSENTYVK 120
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Db 181 KSKTLPFLSMQYSEBFRIHFTFKFQNNPNRSLVKPITQLIGRTHATGIRKVVRELEN 240
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Db 241 ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTQTGSSSFEHMSQEGFSAIT 360
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QY 361 SNGPILLSVGSYDAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNVRQSLV 420
Db 361 SNGPILLSVGSYDAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNVRQSLV 420
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601	Db	DLTVGAQGHVLLBSQPVLRYKATWENPREVARNVFECNDQVYKGEAGBRVCLHVQK	660
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781	Qy	LSITFSFMSLDCLVGGPREPNVTVVRNDCGDSYRTQVTFPPFPDLDSYRKVSTLQORS	840
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841	Qy	QSRWRLACESASSTEVSALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKA	900
841	Db	QSRWRLACESASSTEVSALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKA	900
901	Qy	NVTSENMPRNKTEFOLELVPKYAVYVMVTVSHGVSTKYLNFNTASENISRVMQHOYQVSN	960
901	Db	NVTSENMPRNKTEFOLELVPKYAVYVMVTVSHGVSTKYLNFNTASENISRVMQHOYQVSN	960
961	Qy	LGQRSPLTISLVLPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSHSDFLAELRKAPV	1020
961	Db	LGQRSPLTISLVLPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSHSDFLAELRKAPV	1020
1021	Qy	VNCISIAVCQRIOCDIPFGIOEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDSVF	1080
1021	Db	VNCISIAVCQRIOCDIPFGIOEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDSVF	1080
1081	Qy	TLLPGQGFVRSQETKVEPEVENPPLPLIIVGSSVGGLLLLALITAALYKLGFFKRYOKD	1140
1081	Db	TLLPGQGFVRSQETKVEPEVENPPLPLIIVGSSVGGLLLLALITAALYKLGFFKRYOKD	1140
1141	Qy	MMSBGGPPGABPQ	1153
1141	Db	MMSBGGPPGABPQ	1153

RESULT 4

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US-08-322-652-3
; Sequence 3, Application US/0832652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integer
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
; STREET: 233 South Wacker Drive, 6300 Sour Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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Db 601 DLTVGAQGHVLLRSQPLRVKAIEMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVYDIALDSGRPHSRAVFNETKNSRRQTQVLGTQTCTETLKQLP 720
Db 661 STRDLREGQIQSVVYDIALDSGRPHSRAVFNETKNSRRQTQVLGTQTCTETLKQLP 720
QY 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPPFEKNCNDNICQDD 780
Db 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPPFEKNCNDNICQDD 780
QY 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNRK 840
Db 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNRK 840
QY 841 QRSWLACESASSTEVSGALKSTCSINHPIPFENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTCSINHPIPFENSEVTFNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTBFQLELPKYAVYVVTSHGVSTKYLNTASENTSRVMOHQYQVSN 960
Db 901 NVTSENMPRTNKTBFQLELPKYAVYVVTSHGVSTKYLNTASENTSRVMOHQYQVSN 960
QY 961 LGQRSPLSLVFLVPVRLNQTVIDRPOVTFSENLSSTCHTKERLPSSHDSDFLAELRKAPV 1020
Db 961 LGQRSPLSLVFLVPVRLNQTVIDRPOVTFSENLSSTCHTKERLPSSHDSDFLAELRKAPV 1020
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Db 1021 VNCISIAVCQRIQCDIPFFGQIEFNATLKGNI-SFDWYIKTSHNHLIIVSTABILFNDVSF 1080
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Db 1081 TLLPQGGAFVRSQTKVEPFPVNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKRYQKD 1140
QY 1141 MMSEGGPPGABPQ 1153
Db 1141 MMSEGGPPGABPQ 1153

RESULT 5
US-08-605-672-3
; Sequence 3, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-605-672-3

Query Match 100.0%; Score 5953; DB 2; Length 1153;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIIVAANOR 60
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Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQQLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFGNLRQOQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVFSTVMEOL 180
Db 121 GLCFLFGNLRQOQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVFSTVMEOL 180
QY 181 KKSRTLFLSMQYSEEFTHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFPN 240
Db 181 KKSRTLFLSMQYSEEFTHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFPN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPPRDHVQVNNFEALKTQONQRKXFALEGQTGSSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPPRDHVQVNNFEALKTQONQRKXFALEGQTGSSSSFEHMSQEGFSAAIT 360
QY 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLV 420
Db 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLV 420
QY 421 LGAPRYQHIGLVAMFRQNTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMFRQNTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYEQTRGGQVSVCPPLPRGQARWQCDALVIGEQQPWRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYEQTRGGQVSVCPPLPRGQARWQCDALVIGEQQPWRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
Db 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPLRVKAIEMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPLRVKAIEMFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVYDIALDSGRPHSRAVFNETKNSRRQTQVLGTQTCTETLKQLP 720
Db 661 STRDLREGQIQSVVYDIALDSGRPHSRAVFNETKNSRRQTQVLGTQTCTETLKQLP 720
QY 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPPFEKNCNDNICQDD 780
Db 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPPFEKNCNDNICQDD 780

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Db 781 LSITFSMSLDCLVVGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
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Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
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Db 901 NVTSENMPRTNKTEFOLELPVKYAVYVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960
Qy 961 LGQSLPISLVFLVRLNQTVINDRPOVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Db 961 LGQSLPISLVFLVRLNQTVINDRPOVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Qy 1021 VNCSTAVCORIQCDIPFFGIQBEFNATLKGMLSPDWYIKTSHNHLIVSTAEIILFNDVSF 1080
Db 1021 VNCSTAVCORIQCDIPFFGIQBEFNATLKGMLSPDWYIKTSHNHLIVSTAEIILFNDVSF 1080
Qy 1081 TLLPQOGAFVRSQETKVEPEVPNPLPIVGVSSVGGILLALITAALYKLGFFKROYKD 1140
Db 1081 TLLPQOGAFVRSQETKVEPEVPNPLPIVGVSSVGGILLALITAALYKLGFFKROYKD 1140
Qy 1141 NMSEGGPPGABPQ 1153
Db 1141 NMSEGGPPGABPQ 1153

RESULT 6

US-08-482-293A-3
; Sequence 3, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-293A-3
Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAURVLLLTALTTLCHGNLDTENAMTFQENARGQSVVQLQGSRRVVGAPQEIIVANQR 60
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Db 61 GSLVQCDSYSGSCPIRLQVPVEAVNMSLGLSLAATTPPOLLAGCTVPTVHQTCSNTYVK 120
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Db 361 SNGPLSTVGSYDWAGGVFLYTSKEKSTFINMTVDSDMDNDAYLGAAAAIILNRVQSLV 420
Qy 421 LGAPRYOHIGLVAMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYOHIGLVAMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYEQTREGQVSVCLPRGQARWQCDAVLYGEGQGPWRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYEQTREGQVSVCLPRGQARWQCDAVLYGEGQGPWRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPLQYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPLQYFGQSLSGGQDLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVOK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGEAGEVRVCLHVOK 660
Qy 661 STRDLREGQIQSVVTVYDLALDSDGRPHSRVAVNETKSTRQTVGLGTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVVTVYDLALDSDGRPHSRVAVNETKSTRQTVGLGTQTCETLKLQLP 720
Qy 721 NCIEDPVSPIVLRNLSIAGTGLSAFNLRLVLAEDAQRLLFTALFPPEKNCNDNICODD 780
Db 721 NCIEDPVSPIVLRNLSIAGTGLSAFNLRLVLAEDAQRLLFTALFPPEKNCNDNICODD 780
Qy 781 LSIITFSFMSLDCLVVGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Db 781 LSIITFSFMSLDCLVVGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Qy 901 NVTSENMPRTNKTEFOLELPVKYAVYVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960

Db 901 NVTSENNPRTNKTBFQLELPVKYAVYVMVSHGVSTKYLNTFASENTSRVMOHQYQVSN 960
QY 961 LGQRLPISLVFLVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSSHDSDFLAELRKAPV 1020
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Db 1081 TLLPGQAFVRSQTKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEQ 1153
Db 1141 MMSEGGPPGAEQ 1153

RESULT 7

US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3

Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLILTALTTLCHGFNLDTENAMTFQENARGFQCSVVQLQGSRRVVVVGAPQEI VAAQR 60
Db 1 MALRVLILTALTTLCHGFNLDTENAMTFQENARGFQCSVVQLQGSRRVVVVGAPQEI VAAQR 60
QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLAGCPTVHTCSENTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLAGCPTVHTCSENTYVK 120
QY 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDAFLIDGSGSIIPHDFRRKMFVSTMEOL 180
Db 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDAFLIDGSGSIIPHDFRRKMFVSTMEOL 180
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Db 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLIGRTHATIGIKVVRLEFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
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Db 301 NTIASKPPRDHVFQVNNFEALKTIQNLREKXFALEGTTGSSSSFEHMSOEGFSAAT 360
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Db 361 SNGPLLLSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
QY 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
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Db 481 HYYEOTRGQGVSVCPPLRGQARWQCDAVLGEQCPMRFGAALTVLGDVNGDKLTQVA 540
QY 541 IGAPGEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFQCSLGGQDLTMDGLV 600
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QY 601 DLTVGAQGHVLLRLSQPVLRVKAIMEFNPVARNVFNCDQVVKGKBAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRLSQPVLRVKAIMEFNPVARNVFNCDQVVKGKBAGEVRVCLHVQK 660
QY 661 STRDLREGQIOSVVTYDLALDSGPHSRVAFNETKNSTRQTQVLGTQTCETIKLQLP 720
Db 661 STRDLREGQIOSVVTYDLALDSGPHSRVAFNETKNSTRQTQVLGTQTCETIKLQLP 720
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Db 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNRPVLAEDAQRLFTALPFFKNCNDNI CQDD 780
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Db 781 LSITFSPMSLDCLVVGGRPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRS 840
QY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIEPENSEVTNITFPDVS KASLGNKLLKA 900
Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIEPENSEVTNITFPDVS KASLGNKLLKA 900
QY 901 NVTSENNPRTNKTBFQLELPVKYAVYVMVSHGVSTKYLNTFASENTSRVMOHQYQVSN 960
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QY 1081 TLLPQCGAFVRSQETKVEPEVFNPLPLIYGVSSVGGLLALITAAALYKLGFFKQYKD 1140
Db 1081 TLLPQCGAFVRSQETKVEPEVFNPLPLIYGVSSVGGLLALITAAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEPO 1153
Db 1141 MMSEGGPPGAEPO 1153
RESULT 8
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; FILE OF INVENTION: No. 6251395el Human 2
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3
Query Match 100.0%; Score 5953; DB 3; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRVLLLTALTLCHGFNLDENAMTFQENARGFQGVVQLOGSRVVVVGAPQEIIVAAQR 60
Db 1 MALRVLLLTALTLCHGFNLDENAMTFQENARGFQGVVQLOGSRVVVVGAPQEIIVAAQR 60
QY 61 GSYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTGPPOLLACGPTVHOTSNTYVK 120
Db 61 GSYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTGPPOLLACGPTVHOTSNTYVK 120
QY 121 GLCFLFGSNLRQOPKQFPALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMBOL 180
Db 121 GLCFLFGSNLRQOPKQFPALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMBOL 180
QY 181 KSKTLFSLMOYSEFRHTFKEFQNNPNRSLVKPIITOLLGRTHATGIRKVVRELFN 240
Db 181 KSKTLFSLMOYSEFRHTFKEFQNNPNRSLVKPIITOLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKTLVITDGEKFDPLGVEDVITPEADREGVIRVYGVGDAPRSEKSRQEL 300
Db 241 ITNGARKNAFKTLVITDGEKFDPLGVEDVITPEADREGVIRVYGVGDAPRSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNFEALXTIQNLRKXFAIEGTGTGSSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPRDRHVQVNNFEALXTIQNLRKXFAIEGTGTGSSSSFEHMSQEGFSAAIT 360
QY 361 SNGPILLSTVGSVDMAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNRVQSLV 420
Db 361 SNGPILLSTVGSVDMAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNRVQSLV 420
QY 421 LGAPRYQHILGVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHILGVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYEOTRGQSVSVCPLPRGQARWQCDVLYGEOQGPWGRFGAALTIVLGDVNGDKLTDVA 540

Db 481 HYYEOTRGQSVSVCPLPRGQARWQCDVLYGEOQGPWGRFGAALTIVLGDVNGDKLTDVA 540
QY 541 IGAPGEEDNRGAVLFGHTSGSISPSHSORISAGSKLSPLQYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLFGHTSGSISPSHSORISAGSKLSPLQYFGQSLSGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPLRVKAIMBENPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPLRVKAIMBENPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVTDLALDSGRPHSRVAVNFNTRKSTRQTOVLGLTQTCETILKQLP 720
Db 661 STRDLREGQIQSVVTDLALDSGRPHSRVAVNFNTRKSTRQTOVLGLTQTCETILKQLP 720
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Db 721 NCIEDPVSPIVLRNLSVGTPLSAFGLNRLPVLAEADQRLFTALFPPEKNCNNDNICODD 780
QY 781 LSITFSFMSLDCLVVGPPREFNVTVTVRNDGEDSYRTQVTFPPFPLDLSYRKVSTLQORS 840
Db 781 LSITFSFMSLDCLVVGPPREFNVTVTVRNDGEDSYRTQVTFPPFPLDLSYRKVSTLQORS 840
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Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMOHQYQVSN 960
Db 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMOHQYQVSN 960
QY 961 LGQSLPISLVFLVPLNQTIVWDRPQVTFSENLSTCHTKERLPSHSDFLAELRKAPV 1020
Db 961 LGQSLPISLVFLVPLNQTIVWDRPQVTFSENLSTCHTKERLPSHSDFLAELRKAPV 1020
QY 1021 VNCIAVCORIQCDDIPFGIOEBFNATLKGNSLFDWIKTSHNHLIIVSTAEILFNDVSF 1080
Db 1021 VNCIAVCORIQCDDIPFGIOEBFNATLKGNSLFDWIKTSHNHLIIVSTAEILFNDVSF 1080
QY 1081 TLLPQCGAFVRSQETKVEPEVFNPLPLIYGVSSVGGLLALITAAALYKLGFFKQYKD 1140
Db 1081 TLLPQCGAFVRSQETKVEPEVFNPLPLIYGVSSVGGLLALITAAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEPO 1153
Db 1141 MMSEGGPPGAEPO 1153
RESULT 9
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; FILE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 3																																																
; LENGTH: 1153																																																
; TYPE: PRT																																																
; ORGANISM: Homo sapiens																																																
US-09-688-307A-3																																																
Query Match 100.0%; Score 5953; DB 4; Length 1153;																																																
Best Local Similarity 99.9%; Pred. No. 0;																																																
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;																																																
Qy	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQ	EIVAA	NOR 60																																						
Db	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQ	EIVAA	NOR 60																																						
Qy	61	GSLYQCDYST	GCEPIRLQ	VPVEAV	NMSLGL	SLAAT	TPPQL	LACG	PTVH	QCS	ENTYVK 120																																					
Db	61	GSLYQCDYST	GCEPIRLQ	VPVEAV	NMSLGL	SLAAT	TPPQL	LACG	PTVH	QCS	ENTYVK 120																																					
Qy	121	GLCFLFGS	NLRQOP	KFP	PEALRG	CCQ	EDSDIA	FLID	SGSII	PHD	FRMK	EFV	STV	MEQL 180																																		
Db	121	GLCFLFGS	NLRQOP	KFP	PEALRG	CCQ	EDSDIA	FLID	SGSII	PHD	FRMK	EFV	STV	MEQL 180																																		
Qy	181	KSKTFL	SLMOY	SEFR	IHFT	FK	QNNP	NRSL	VKPT	IT	QLGR	TH	TATG	IRK	VV	REL	FN 240																															
Db	181	KSKTFL	SLMOY	SEFR	IHFT	FK	QNNP	NRSL	VKPT	IT	QLGR	TH	TATG	IRK	VV	REL	FN 240																															
Qy	241	ITNGARK	NAFKIL	VVIT	DG	KFGD	PL	GY	ED	VI	PE	AD	REG	VI	RY	VI	GV	GD	AF	SE	KSR	Q	REL 300																									
Db	241	ITNGARK	NAFKIL	VVIT	DG	KFGD	PL	GY	ED	VI	PE	AD	REG	VI	RY	VI	GV	GD	AF	SE	KSR	Q	REL 300																									
Qy	301	NTIASK	PRDRH	VFQ	NN	FEAL	KTION	Q	RE	KY	FA	IE	G	T	Q	TG	SS	SS	FE	H	MS	Q	E	G	S	A	A	I	T 360																			
Db	301	NTIASK	PRDRH	VFQ	NN	FEAL	KTION	Q	RE	KY	FA	IE	G	T	Q	TG	SS	SS	FE	H	MS	Q	E	G	S	A	A	I	T 360																			
Qy	361	SNGPLLSTVGS	YDWAGGV	FLYTS	KEKST	PT	IN	TR	VDS	MND	AYL	G	Y	A	A	I	L	R	N	R	V	Q	S	L	V 420																							
Db	361	SNGPLLSTVGS	YDWAGGV	FLYTS	KEKST	PT	IN	TR	VDS	MND	AYL	G	Y	A	A	I	L	R	N	R	V	Q	S	L	V 420																							
Qy	421	LGAPRYQHIGL	VAMFRQNT	GMWES	NAN	VKG	TQ	I	G	A	F	G	A	S	L	C	S	D	V	D	S	N	G	S	T	D	L	V	L	I	G	A	P 480															
Db	421	LGAPRYQHIGL	VAMFRQNT	GMWES	NAN	VKG	TQ	I	G	A	F	G	A	S	L	C	S	D	V	D	S	N	G	S	T	D	L	V	L	I	G	A	P 480															
Qy	481	HYEOTRGGQV	SVCP	PL	PR	Q	R	A	R	W	C	D	A	V	L	Y	E	Q	O	Q	P	W	R	F	G	A	L	T	V	L	G	D	V	N	G	D	K	L	T	D	V	A 540						
Db	481	HYEOTRGGQV	SVCP	PL	PR	Q	R	A	R	W	C	D	A	V	L	Y	E	Q	O	Q	P	W	R	F	G	A	L	T	V	L	G	D	V	N	G	D	K	L	T	D	V	A 540						
Qy	541	IGAPGEDNRGA	VYLL	PHGT	SGSGI	SP	SH	S	O	R	T	A	G	S	K	L	S	P	R	O	Y	F	G	O	S	L	G	G	D	I	T	M	D	G	L	V 600												
Db	541	IGAPGEDNRGA	VYLL	PHGT	SGSGI	SP	SH	S	O	R	T	A	G	S	K	L	S	P	R	O	Y	F	G	O	S	L	G	G	D	I	T	M	D	G	L	V 600												
Qy	601	DLTVGAQGHV	LLLR	SP	VL	R	V	L	R	V	K	A	I	M	E	F	N	P	R	V	A	R	N	V	F	E	C	N	D	O	V	K	G	E	A	G	E	R	V	C	L	H	V	Q	K 660			
Db	601	DLTVGAQGHV	LLLR	SP	VL	R	V	L	R	V	K	A	I	M	E	F	N	P	R	V	A	R	N	V	F	E	C	N	D	O	V	K	G	E	A	G	E	R	V	C	L	H	V	Q	K 660			
Qy	661	STRDRLREGQI	OSV	VT	Y	D	I	A	L	S	G	R	H	S	R	A	V	N	E	T	K	N	S	T	R	Q	T	V	L	G	T	Q	C	E	T	L	K	I	Q	L	P 720							
Db	661	STRDRLREGQI	OSV	VT	Y	D	I	A	L	S	G	R	H	S	R	A	V	N	E	T	K	N	S	T	R	Q	T	V	L	G	T	Q	C	E	T	L	K	I	Q	L	P 720							
Qy	721	NCIEDVPSP	VL	R	N	F	S	L	G	T	P	L	S	A	F	G	N	L	R	P	V	L	A	E	D	A	O	R	L	T	A	L	P	P	E	K	N	C	G	N	D	I	C	O	D	780		
Db	721	NCIEDVPSP	VL	R	N	F	S	L	G	T	P	L	S	A	F	G	N	L	R	P	V	L	A	E	D	A	O	R	L	T	A	L	P	P	E	K	N	C	G	N	D	I	C	O	D	780		
Qy	781	LSITTFMS	LDCL	V	G	G	P	R	E	F	N	V	T	V	R	N	D	G	E	D	S	V	R	T	O	V	T	F	F	P	L	D	L	S	Y	R	K	V	S	T	L	Q	N	R	S 840			
Db	781	LSITTFMS	LDCL	V	G	G	P	R	E	F	N	V	T	V	R	N	D	G	E	D	S	V	R	T	O	V	T	F	F	P	L	D	L	S	Y	R	K	V	S	T	L	Q	N	R	S 840			
Qy	841	QRSWRLACES	AS	T	E	V	S	G	A	L	K	T	S	C	S	I	N	H	P	I	P	E	N	S	E	V	T	F	N	I	T	D	V	D	S	K	A	S	L	G	N	K	L	L	K	A 900		
Db	841	QRSWRLACES	AS	T	E	V	S	G	A	L	K	T	S	C	S	I	N	H	P	I	P	E	N	S	E	V	T	F	N	I	T	D	V	D	S	K	A	S	L	G	N	K	L	L	K	A 900		
Qy	901	NVTSENMP	TR	N	K	T	E	F	O	L	E	P	L	P	V	K	I	A	V	M	V	T	S	H	G	V	T	K	I	N	F	T	A	S	E	N	T	S	R	V	M	O	Q	Y	O	V	S	N 960
Db	901	NVTSENMP	TR	N	K	T	E	F	O	L	E	P	L	P	V	K	I	A	V	M	V	T	S	H	G	V	T	K	I	N	F	T	A	S	E	N	T	S	R	V	M	O	Q	Y	O	V	S	N 960

Db 301 NTIASKPPDRHVQVNNFEALKTQNLREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGPLLSVGSYDAGGVLTSKEKSTFINWTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Db 361 SNGPLLSVGSYDAGGVLTSKEKSTFINWTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYEQTRGGQSVVCLPRGQARWQCDVAVLGEQCPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYEQTRGGQSVVCLPRGQARWQCDVAVLGEQCPWGRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPCEDNRGAVILFHTGSSGISPSHSQRIAGSKLSPRLOYFGOSLGGODLTMDGLV 600
Db 541 IGAPCEDNRGAVILFHTGSSGISPSHSQRIAGSKLSPRLOYFGOSLGGODLTMDGLV 600
Qy 601 DLTGAQGHVLLLRQPVLRVKAIMEFNPREVARNVFCNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTGAQGHVLLLRQPVLRVKAIMEFNPREVARNVFCNDQVVKGEAGEVRVCLHVQK 660
Qy 661 STRDLRGQIQSVVTVYDALDGRPHSRVAFNETKNSRTRQTVGLTQTCETLKLQLP 720
Db 661 STRDLRGQIQSVVTVYDALDGRPHSRVAFNETKNSRTRQTVGLTQTCETLKLQLP 720
Qy 721 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPPEKNCNDNICODD 780
Db 721 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPPEKNCNDNICODD 780
Qy 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNRS 840
Db 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNRS 840
Qy 841 QRSWLACESASSTEVSGALKSTCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Qy 901 NVTSENNPRTNKTBFQLELPVKYAVVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960
Db 901 NVTSENNPRTNKTBFQLELPVKYAVVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960
Qy 961 LGQSLPISLVLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Db 961 LGQSLPISLVLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Qy 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLIIVSTABILFNDVSF 1080
Db 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLIIVSTABILFNDVSF 1080
Qy 1081 TLLPGQGFVRVRSOTETKVEPFPVNPPLIVGVSSVGGLLLALITAAALYKLGFFKRYQKD 1140
Db 1081 TLLPGQGFVRVRSOTETKVEPFPVNPPLIVGVSSVGGLLLALITAAALYKLGFFKRYQKD 1140
Qy 1141 NMSEGGPPGAEQ 1153
Db 1141 NMSEGGPPGAEQ 1153

RESULT 11
US-08-476-062A-43
; Sequence 43, Application US/08476062A
; Patent No. 587275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-476-062A-43

Query Match 99.5%; Score 5922.5; DB 2; Length 1152;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1149; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MALRVLLLTALTLCCHGNLDNENAMTFQENARGQSVVQLQSGRVVVGAPQEIIVANQR 60
Db 1 MALRVLLLTALTLCCHGNLDNENAMTFQENARGQSVVQLQSGRVVVGAPQEIIVANQR 60
Qy 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPSPOLLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPSPOLLACGPTVHQTCSNTYVK 120
Qy 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMSQL 180
Db 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMSQL 180
Qy 181 KSKTILFSLMOYSEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Db 181 KSKTILFSLMOYSEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVGDAPRSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVGDAPRSEKSRQEL 300
Qy 301 NTIASKPPDRHVQVNNFEALKTQNLREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPPDRHVQVNNFEALKTQNLREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGPLLSVGSYDAGGVLTSKEKSTFINWTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Db 361 SNGPLLSVGSYDAGGVLTSKEKSTFINWTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYEQTRGGQSVVCLPRGQARWQCDVAVLGEQCPWGRFGAALTVLGDVNGDKLTDVA 540

Db 481 HYEOTRGQVSVCLPRG-RARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDA 539
QY 541 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 540 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
QY 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 600 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 659
QY 661 STRDLREGQIOSVVTYDLALDSGRPHRAVNETKNSRRTOTVGLTQTCETLKLQLP 720
Db 660 STRDLREGQIOSVVTYDLALDSGRPHRAVNETKNSRRTOTVGLTQTCETLKLQLP 719
QY 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAORLFTALPFFKNCNDNICQDD 780
Db 720 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAORLFTALPFFKNCNDNICQDD 779
QY 781 LSITFSMSLDCLVGGPREFNVTVVRNDGDSYRTQVTFPPDLDSYRKVSTLQORS 840
Db 780 LSITFSMSLDCLVGGPREFNVTVVRNDGDSYRTQVTFPPDLDSYRKVSTLQORS 839
QY 841 QRSWLACESASTVSGALKSTCSINHIPIPPENSEVTFNITDVSASIGNKLLKA 900
Db 840 QRSWLACESASTVSGALKSTCSINHIPIPPENSEVTFNITDVSASIGNKLLKA 899
QY 901 NVTSENPRNTKTEFQLELPKYAVVTVTSHGVSTKYLNFTASENTSRVNHQYQVSN 960
Db 900 NVTSENPRNTKTEFQLELPKYAVVTVTSHGVSTKYLNFTASENTSRVNHQYQVSN 959
QY 961 LGQSLPSLVPLVRLNQTWIDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
Db 960 LGQSPFISLVPLVRLNQTWIDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1019
QY 1021 VNCSTAVCORIOCDIPFGIQEFNATLKGNIUSDWYIKTSHNHLIIYSTABILFNDVSF 1080
Db 1020 VNCSTAVCORIOCDIPFGIQEFNATLKGNIUSDWYIKTSHNHLIIYSTABILFNDVSF 1079
QY 1081 TLLPQOGAFVRQOTETKVEPFPVNPPLPLIVGSSVGGILLLALITAAALYKLGFFRKQYKD 1140
Db 1080 TLLPQOGAFVRQOTETKVEPFPVNPPLPLIVGSSVGGILLLALITAAALYKLGFFRKQYKD 1139
QY 1141 MMSEGGPPGAEPQ 1153
Db 1140 MMSEGGPPGAEPQ 1152

RESULT 12

PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaut
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fieh & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167

; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US96-01314-43

Query Match 99.5%; Score 5922.5; DB 5; Length 1152;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1149; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQSVVQLQGSRVVVGAPQEIIVAANQR 60
Db 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQSVVQLQGSRVVVGAPQEIIVAANQR 60
QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSENTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSENTYVK 120
QY 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEOL 180
Db 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEOL 180
QY 181 KSKTLPFSLMOYSEFRHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
Db 181 KSKTLPFSLMOYSEFRHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFSEKSRQEL 300
QY 301 NTIASKPPRDHVQVNNFEALKTIONQREKFAIECTGTGSSSSFEHMSQEGFSAAT 360
Db 301 NTIASKPPRDHVQVNNFEALKTIONQREKFAIECTGTGSSSSFEHMSQEGFSAAT 360
QY 361 SNGPLLSVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
Db 361 SNGPLLSVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMPRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYEOTRGQVSVCLPRGQARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDA 540
Db 481 HYEOTRGQVSVCLPRG-RARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDA 539
QY 541 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 540 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
QY 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 600 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 659
QY 661 STRDLREGQIOSVVTYDLALDSGRPHRAVNETKNSRRTOTVGLTQTCETLKLQLP 720
Db 660 STRDLREGQIOSVVTYDLALDSGRPHRAVNETKNSRRTOTVGLTQTCETLKLQLP 719
QY 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAORLFTALPFFKNCNDNICQDD 780
Db 720 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAORLFTALPFFKNCNDNICQDD 779


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; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-062A-44

Query Match      58.8%; Score 3500; DB 2; Length 1163;
Best Local Similarity 61.3%; Pred. No. 2.3e-279;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLTALTALCHGNLDNENAMTFQSNARGFGVQVQLQGSRRVVGAPQBIIVAAVNRGSLY 64
DB 8 LLLFTALATSLGFLNDTBEITAFRVDSDAGFSDGVQVYANVWVVGAPQKITAANTGGLY 67
QY 65 QCDYSTGCEPIRLQVPEAVNMSLGLSLAATSPQLLACGPTVHQCSTENYVYGLCF 124
DB 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLAATSPQLLACGPTVHHECGRNMYLTGLCF 127
QY 125 LFGSNLRQOPKFPALRGCPQEDSDIAFLIDGSGIIPHDPRMKEFVSTVMEQLKSK 184
DB 128 LLGPT--QLTQRLPVSRQECPRQEQDIVFLIDGSGISSRNPFATWVNFVRAVISQFRPS 185
QY 185 TLFLSLMOYSEBPIHFTPKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNG 244
DB 186 TQFLSLMQFSNKEQTFTFEFRPTNSPLSLASVHQLQGFYTATATQVNVHRLPHASVG 245
QY 245 ARKNAFKILVITDGEKFDPLGYDVIPEADREGVIRYVIGVGDAFRSEKSRQBLNTIA 304
DB 246 ARRDATKILVITDCKEGLSDYKDVIPMDAAGIIRYAGVGLAFQNRNSWKLNDIA 305
QY 305 SKPPRDHVFQVNNFALKTIQNLREKFAIPAGTGTGSSSSFEHEMSQEGFSAALTSNCP 364
DB 306 SKPSQEHIFKVDFFDALKDQNLREKFAIPAGTGTGSSSSFEHEMSQEGFSAVTPDGP 365
QY 365 LLSTVGSVDWAGGVLYTSKESKSTFNTRVDSDDNDVGLVYAAAIILRNVRQSVLVLGAP 424
DB 366 VLAVGSGFTWSGAFLYPPNMGPTFNMSQVNDVMDRSDYLGSTELALWKGVSQSVLVLGAP 425
QY 425 RYQHILGLVAMFRQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSTDVLVLGAPHYIE 484
DB 426 RYQHTGKAVIFTQVSRQWRMKAETVGTQIGSYFGASLCSVDVDTGSTDVLVLGAPHYIE 485
QY 485 QTRGGQVSVCPPLPRGWR--RWCDDAVLYGEQQHPWGRFGAALTVLGDVNGDKLTVVIGAP 544

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DB 486 QTRGGQVSVCPPLPRGWR--RWCDDAVLYGEQQHPWGRFGAALTVLGDVNGDKLTVVIGAP 544
QY 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPLQYFQGSQSGQDLTMDGLVDLT 604
DB 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPLQYFQGSQSGQDLTMDGLVDLT 604
QY 605 GAQGHVLLRSQPLRVKAIMFNPVREVARNVFECNDQVVGKEAGEVRVCLHVOKSTRD 664
DB 605 GARGQVLLLRTRPVLWVGSMQFIPAEIPRSAFECEQVSEQTLVQSNICLYIDKRSKN 664
QY 665 RLREGQIOSVVTYDLALDSGRPHSAVENFNKSNRRROTQVLGLTQTCTETLKLQPCNIE 724
DB 665 LLGSRDLQSSVTLDLALDPGRSLPRATEQETKNSLSRVRLGLKAKHCFNLLPLPSCVE 724
QY 725 DPVSPVILRLNFSLVGTPLSFAFGLNLRPVLAEDAQRALTALPFFERNKNDNINCQDLSIT 784
DB 725 DSVTPITLRLNFTLVGKELLAFRLNLRPMLAALQRYFTASLPFFERNKCGADHICQDNLGIS 784
QY 785 FPFMSLDCLVGGPREFNVTVVRNDGEDSDTRTQVTFPFLDLSYRKVSTLQNRQSRW 844
DB 785 FSPFGLKSLVGSNLELNARVWVWMDGEDSDYGTITTFSSHAPAGLSYRYVAEGQKQQLRSL 844
QY 845 RLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITEDVDSKASLGNKLLKANVTS 904
DB 845 HLTCDSPVG--SQGTWSTSCRINHLPGRGAQITFLATFDVSPKAVJGDRLLLTANVSS 902
QY 905 ENNMPRTNKTEFQLELPVKYAVYVVTSHGVSTKYLNFTAS--ENTSRVMOHQYVSNLQ 963
DB 903 ENNTPRTSKTTFQLELPVKYAVYVVTSSHEQFTKYLNFESESEKESHVAMHRYQVNNLQ 962
QY 964 RSLPISLVPLVRLNQVWDRPQVTFSENLSSTCTHYKERLPSHSDFLAEURKAPVNC 1023
DB 963 RDLPVSIINFVPELVQEAQVWMDVEVSHVQNPSPSLRCSSEKIAAPPASDFLAHTKQNPVLD 1022
QY 1024 SIACQRTQCDIPRFGIOEFENATLKNLSFDWYIKTSHNHLIIVSTAEILFNDVSFTLL 1083
DB 1023 SIAGLRFCRCDVPSFVQEEELDTLKGNSLFGWQVLIQKVKVSVSVAEITPDTVSISQL 1082
QY 1084 PQGAFVRSQTSQTVKPEPPEVNPPLIIVGSSVGGLLLLALITAALYKLGFFKRYKQKMM 1143
DB 1083 PQGAFVRSQTSQTVKPEPPEVNPPLIIVGSSVGGLLLLALITAALYKLGFFKRYKQK 1142
QY 1144 E 1144
DB 1143 E 1143

RESULT 15
PCT-US96-01314-44
; Sequence 44, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95

```


ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1163
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-01314-44

Query Match 58.8%; Score 3500; DB 5; Length 1163;
Best Local Similarity 61.3%; Pred. No. 2.3e-279;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;
PCT 5 LLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRRVVGAPQBIIVANORGSLY 64
DB 8 LLLTALATSLGFLNLTDELTAFRVDSDAGFQSVVQYANVWVVGAPQKITAANTGGGLY 67
QY 65 QCDYGTGSCPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVKGGLCF 124
DB 68 QCGYSTGACEPIGLQVPPPEAVNMSLGLSLASTTSPQLLACGPTVHHECGRNMYLTGLCF 127
QY 125 LFGSNLRQOPKFPALRGCPEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSK 184
DB 128 LIGPT--QLTQLPVSQRCPQEQDIFLIDGSGSISRNFATWVNFVRAVISQFORPS 185
QY 185 TLFLSMQVSEEPRIHFTPKFQNNPNRSLVKPITQQLGRTHTATGIRKVVRELFENITNG 244
DB 186 TQFSLMQFSNKQTHFTFEFRPTNPLSLASVHQLQGFYTTATAIQNVHRLFHASYG 245
QY 245 ARKNAFKILVITDGEKFDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIA 304
DB 246 ARRDATKILVITDGEKGSLOYKDVIPMDAAGIIRYVIGVGLAFQNRNSWKELNDIA 305
QY 305 SKPPRDHVFQVNNFEALKTIQNLREKFAIBGTQGTSSSFEHEMSQEGFSAATISNGP 364
DB 306 SKPSQEHIPKVEDFDALKDIOQLREKFAIBGTETSSSFELEMAQEGFSAVFTPDGP 365
QY 365 LLSTVGSVDWAGGFVLYTSKEKSTFINMTRVDSMDNDAYLGYAAAIILNRVQSLVGLAP 424
DB 366 VLGAQVSTWSGGAFLYPNMSPFINMSQENVMDSDYLGYSTELALWKGVSQSLVGLAP 425
QY 425 RYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSDVDVDSNGSTDLLVIGAPHYIE 484
DB 426 RYQHTGKAVIFTQVSRQWRMKAETVGTQIGSYFGASLCSDVDVDTGSTDLLVIGAPHYIE 485
QY 485 QTRGGQVSVCPPLPRQARWQCDVLYGEOGPWGRFGAALTIVLGDVNGDKLTDVIGAP 544
DB 486 QTRGGQVSVCPPLPRGWR-RWVCDVLYGEOGPWGRFGAALTIVLGDVNGDKLTDVIGAP 544
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DB 545 GEEENRGAVLPHGVLPSPISPSHSORAGSKLSPRLQYFGQALSGGQDLTQDGLVDLAV 604
QY 605 GAQGHVLLRSQVPLRVKAIMFNPVARNVFECDNVKGEAGEVVRVCLHVQKSTRD 664
DB 605 GARGQVLLLRTPVLMVGVSMQFIPAEIPRSFAFECREQVWSEQTLVQSNICLYIDKRSKN 664
QY 665 RLREGQIGSVTYDLALDGRPHSRVAFNETKSTRTQTVLGLTQTCETLKLQLPNCIE 724
DB 665 LIGSRDLQSSVTLDLALDPGLSPRATFOETKRSLSRVRLGLKAHCENFNLLPSCVE 724
QY 725 DPVSPVLRNLFNPLSAPGNLRPVLAEDAQRLFTALPFPEKNCNDNICODDLISIT 784
DB 725 DSVTPITLRNFTLVGKPLAFNRNPLMALAQRYFTASLPFEKNCADHICQDNLGIS 784
QY 785 F5FMSLDCLVVGGRPFNNVTVTNRDGEDSVYRTQVTFPPFLDLSYKRVSTLQNRQSRW 844

DB 785 FSFPGKSLLVGSNLELNAEVMVWVNDGEDSYGTTITFSGHPAGLSYRYVAEGKQQLRSL 844
QY 845 PLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTS 904
DB 845 HLTCDSPV--SOGTWSSTCRINHILFRGAQITFLATFDVSPKAVILGDRLLLTANVSS 902
QY 905 ENNMPRTNKTFOLELPVKYAVYVWVTSYVSHGYSYTKYLNFTAS-ENTSRVMOHQYOVSNLQ 963
DB 903 ENNTPRTSKTTFQLELPVKYAVYVTSVSHGYSYTKYLNFTAS-ENTSRVMOHQYOVSNLQ 962
QY 964 RSLPISLVFLVPLRINQTVIWRDPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVNC 1023
DB 963 RDLPSVINFWVVELNQEAVMVDEVSHPQNPRLCSSEKIAPPASDDELAHIQKNPVLDC 1022
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DB 1023 SIAGCLRFRCDDVPFSVQOEELDFTLKGNLSFGWVRQILQKKVSVVSVABEITFDTSVYSQL 1082
QY 1084 PGQAFVRSQETETKVEPPEPEVNPPLIVGSSVGGILLALITALYKLGFFKROYKDWMS 1143
DB 1083 PGQAFVRSQETETKVEPPEPEVNPPLIVGSSVGGILLALITALYKLGFFKROYKDWMS 1142
QY 1144 E 1144
DB 1143 E 1143

Search completed: January 13, 2005, 15:34:33
Job time : 61.4108 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 5.47465 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQSDSDIAFLIDGSGSIIP.....FQVNNFEALKTIONQLREKX 189
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	966	100.0	1153	1	RWULB	cell surface glyco
2	746	77.2	1153	2	S0051	leukocyte surface
3	540	55.9	1163	1	RWULC	cell surface glyco
4	328	34.0	1179	2	A5213	integrin alpha-E c
5	287.5	29.8	1170	2	S0330	cell surface glyco
6	261	27.0	1163	2	I56126	lymphocyte fuction
7	242	25.1	493	2	A33809	cartilage matrix p
8	235	24.3	500	2	S66522	cartilage matrix p
9	232	24.0	496	2	A37979	cartilage matrix p
10	215	22.3	3124	2	A40020	collagen alpha 1(X
11	214.5	22.2	1747	2	A45974	collagen alpha 1(X
12	214.5	22.2	1857	2	S31212	collagen alpha 1(X
13	214.5	22.2	1888	2	S78476	collagen alpha 1(X
14	207.5	21.5	1151	2	A45226	integrin alpha-1 c
15	207.5	21.5	3051	2	A43273	hypothetical prote
16	197.5	20.4	272	2	A55348	integrin alpha-1 c
17	192.5	19.9	1180	2	A35854	hypothetical prote
18	191.5	19.8	741	2	T46488	type XII collagen
19	188	19.5	929	2	I51027	collagen alpha 1(V
20	174.5	18.1	2944	2	A54849	collagen alpha 3(V
21	164	17.0	3176	2	CGHU3A	collagen alpha 3(V
22	162	16.8	3137	2	A37797	collagen alpha 2 s
23	159	16.5	1170	2	I45914	integrin alpha-2 c
24	154	15.9	1181	2	A33998	VLA-2 protein homo
25	149	15.4	1178	2	S44142	hypothetical prote
26	146	15.1	550	2	T23760	undulin 1 - human
27	143	14.8	843	2	A40970	collagen alpha 2(V
28	140.5	14.5	371	2	S32604	complement factor
29	136.5	14.1	763	2	I50807	

30	134.5	13.9	712	2	A45638	immunodominant mic
31	132	13.7	2813	1	VWU	von Willebrand fac
32	127.5	13.2	191	2	I47230	VLA-2 protein - pi
33	125.5	13.0	1029	1	S21369	collagen alpha 2(V
34	124.5	12.9	1022	2	S04111	collagen alpha 2(V
35	122.5	12.7	238	2	C35243	collagen alpha 2(V
36	122.5	12.7	917	2	S09646	collagen alpha 2(V
37	122.5	12.7	1018	1	CGHU2A	collagen alpha 2(V
38	119.5	12.4	724	2	A48569	antigen Em100 - B1
39	118.5	12.3	918	2	S23377	collagen alpha 2(V
40	118	12.2	1019	1	A32856	collagen alpha 1(V
41	115.5	12.0	427	2	G00039	von Willebrand fac
42	113.5	11.7	414	2	PS0323	von Willebrand fac
43	112	11.6	764	1	BBHU	complement factor
44	109.5	11.3	567	2	T28797	hypothetical prote
45	109.5	11.3	13055	2	T16580	hypothetical prote

ALIGNMENTS

RESULT 1

RWULB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11B).

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <CR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:G187284; PIDN:AAA59544.1; PID:G307148

A>Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1.

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:G186935; PIDN:AAA5945

A>Note: the authors translated the codon TAC for residue 1129 as Thr

A>Note: part of this sequence, including the amino end of the mature protein, was confirm

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regi

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:G180018; PIDN:AAA58410.1; PID:G553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:8909893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:G189068; PIDN:AAA59903.1; PID:G386975

A>Note: part of this sequence was confirmed by protein sequencing
 J.Fleming, J.C.; Fahh, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
 J. Immunol. 150, 480-490, 1993
 A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in
 n during evolution.
 A:Reference number: A46526; MUID:93123748; PMID:8419480
 A:Accession: A46526
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-499,501-1153 <PLE>
 A:Cross-references: GB:S52227; NID:9263047; PIDN:AB24821.1; PID:9263049
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
 A>Note: sequence extracted from NCBI backbone (NCBI:121963)
 R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
 Biochim. Biophys. Acta 874, 368-371, 1986
 A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
 A:Reference number: A90664; MUID:87076671; PMID:3539202
 A:Accession: A26091
 A:Molecule type: protein
 A:Residues: 17-31 <PIE>
 A:Experimental source: granulocytes
 R:Fahh, H.L.; Roemarin, A.G.; Tenen, D.G.
 Blood 79, 865-870, 1992
 A>Title: Characterization of the myeloid-specific CD11b promoter.
 A:Reference number: I52567; MUID:92144986; PMID:1346576
 A:Accession: I52567
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GB:M84477; NID:gl80184; PIDN:AA51960.1; PID:9553219
 A:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
 C:Genetics:
 A:Gene: ITGAM; CR3A
 A:Cross-references: GDB:120599; OMIM:120980
 A:Map position: 16p11.2-16p11.2
 A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
 C:Superfamily: cell surface glycoprotein Cdlb; von Willebrand factor type A repeat homo
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: cell surface glycoprotein Cdlb #status experimental <MAT>
 F:17-1108/Domain: extracellular #status predicted <EXT>
 F:17-1108/Domain: von Willebrand factor type A repeat homology <VMA2>
 F:148-473/Region: calcium/magnesium binding #status predicted
 F:530-538/Region: calcium/magnesium binding #status predicted
 F:593-601/Region: calcium/magnesium binding #status predicted
 F:1109-1134/Domain: transmembrane #status predicted <TM>
 F:1135-1153/Domain: intracellular #status predicted <INT>
 F:86,240,391,469,693,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 100.0%; Score 966; DB 1; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 1.2e-74;
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPIITQLGTHRTATGIRKVVRELFNTGARNAKFLLVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPIITQLGTHRTATGIRKVVRELFNTGARNAKFLLVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVPEADREGVIRYVIGDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

RESULT 2
 S00551
 leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alpha chain
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: S00551; I59078
 R:Pytela, R.
 EMBO J. 7, 1371-1378, 1988
 A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
 A:Reference number: S00551; MUID:88312584; PMID:3044779
 A:Accession: S00551
 A:Molecule type: DNA
 A:Residues: 1-1153 <PYT>
 A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:G52982; PIDN:CAA30479.1; PID:G52983
 A>Note: the authors translated the codon CAC for residue 569 as Gln
 R:Sastre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
 Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
 A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
 A:Reference number: I59078; MUID:86287312; PMID:2942940
 A:Accession: I59078
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 11-44 <RES>
 A:Cross-references: GB:M14293; NID:gl98993; PIDN:AAA39484.1; PID:G554193
 C:Genetics:
 A:Gene: Mac-1
 C:Superfamily: cell surface glycoprotein Cdlb; von Willebrand factor type A repeat homo
 C:Keywords: cell adhesion; glycoprotein; transmembrane protein
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
 F:148-318/Domain: von Willebrand factor type A repeat homology <VMA2>
 F:1106-1129/Domain: transmembrane #status predicted <TM>

Query Match 77.2%; Score 746; DB 2; Length 1153;
 Best Local Similarity 77.8%; Pred. No. 8.6e-56;
 Matches 147; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPIITQLGTHRTATGIRKVVRELFNTGARNAKFLLVITDGEKFG 120
 DB 204 DFKENPSRSHVSPKLNKRTKTASGIRKVVRELFNTGARNAKFLLVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLDYKDVPEADREGVIRYVIGVGNAPFNKPSRRELDTIASKPAGEHVQVDNFEALNT 323
 QY 181 IQNQLREKX 189
 DB 324 IQNQLQEKI 332

RESULT 3
 RWHULC
 cell surface glycoprotein Cdlc precursor - human
 N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A36584; A35543; S00864
 R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
 J. Biol. Chem. 265, 12750-12751, 1990
 A:Reference number: A36584
 A:Contents: erratum
 A:Accession: A36584
 A:Molecule type: DNA
 A:Residues: 1-1163 <COR>
 A:Cross-references: UNIPROT:P20702
 A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
 R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
 J. Biol. Chem. 265, 2782-2788, 1990
 A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule
 A:Reference number: A35543; MUID:90153906; PMID:2303426
 A:Accession: A35543

A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A>Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166645; PMID:3327687
A:Accession: S00864
A:Molecule type: mRNA
A:Residues: 1-755, 'L', 757-1163 <CO3>
A:Cross-references: GB:M81695; EMBL:Y00093; NID:9487829; PIDN:AAA59180.1; PID:9487830
A>Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD1b) forms a heterodimer with CD1b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:Cross-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:1108-1123/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:161.89,392,697,735,899,939,1050/Binding site: carbohydrate (Aen) (covalent) #status pre
Query Match 55.9%; Score 540; DB 1; Length 1163;
Best Local Similarity 55.6%; Pred. No. 4e-38;
Matches 105; Conservative 35; Mismatches 49; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMQYSEBFRIHFTFK 60
DB 145 CPROQDQIVLIDSGSISRRNFATMNFVRAVISQFORPSQFSLMQFSNKFQTHTFE 204
QY 61 BQNNPNSRLVKPTOLLGRHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 205 EFRRTSNPLSLASVHQLGFTYTTATQNVVHRLFHASYGARRDATKILVITDGEK 264
QY 121 DPLGVEDVPEADREGVIRVIGVDAPFRSEKRSQELNTIASKPPRDHVFVNNEALKT 180
DB 265 DSLDVKDVIPTADAGIIRYALGVGLAQNRNSWELNDIASKPSQEHFKVEDFDALD 324
QY 181 IQNLREKX 189
DB 325 IQNLKEKI 333
RESULT 4
A:Title: Integrin alpha-E chain - human
A:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
R:Shaw, S.K.; Cepke, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A:Reference number: A53213; MUID:94164962; PMID:8119947
A:Accession: A53213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:Cross-references: UNIPROT:P38570; NID:9457244; PID:9457245
C:Genetics:
A:Gene: GDB:ITGAE
A:Cross-references: GDB:330801
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
F:199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
Query Match 34.0%; Score 328; DB 2; Length 1179;
Best Local Similarity 38.8%; Pred. No. 6e-20;
Matches 71; Conservative 42; Mismatches 68; Indels 2; Gaps 1;

QY 6 SDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMQYSEBFRIHFTFKBQ 63
DB 201 TEIAIILIDSGSIDPPDQRAKDFISNNMRNFYKCFECNFALVQYGGVQTEFDLRDSQ 260
QY 64 NNPNRSRLVKPTOLLGRHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFGDPL 123
DB 261 DVMSLARVQNTIQVGSVTKTASAMQHVLDSIFTSHGSRKASKVMVVLTDGGIFEDPL 320
QY 124 GYEDVPEADREGVIRVIGVDAPFRSEKRSQELNTIASKPPRDHVFVNNEALKTQ 183
DB 321 NLTIVINSPKQGVVERFAIGVEBFKSAARTARELNLIASDDETHAFKVTNNYMALDGLLS 380
QY 184 QLR 186
DB 381 KLR 383
RESULT 5
S03308
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA6874
A>Note: part of this sequence was confirmed by protein sequencing
R:Corwell, R.D.; Gollahon, K.A.; Hickette, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) prom
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:130863)
R:Shelley, C.S.; Farokhzad, O.C.; Arnaut, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A:Title: Identification of cell-specific and developmentally regulated nuclear factors th
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:Cross-references: GB:M95609
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 19303-19311, 1993
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NUE>
A:Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
C:Genetics:
A:Gene: GDB:ITGAL; CD11A
A:Cross-references: GDB:119757; OMIM:153370
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <
F:154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 29.8%; Score 287.5; DB 2; Length 1170;
Best Local Similarity 32.8%; Pred. No. 1.8e-16;
Matches 62; Conservative 50; Mismatches 70; Indels 7; Gaps 2;
QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMQYSEBFRIHFTFK 60

Db		150	CIKGNVDLVFLFDGSMISLOPDEFQKILDPKDWKMLNNTSYQFAAVQFSTSYKTEFDPS	209
QY		61	EFQNNPNRSLVKPITQLGSHTHATGIRKVVRELFNITNGARKNAFKILVLWITDGEKG	120
Db		210	DYVWKWDPDALLKHVKHMLLNTFGAINTVATEVPFEELGARPDATAKVLIIITDGE--A	267
QY		121	DPLGYEDVNIPEADREGVTRYVIGVGDAFRSEKSHQELNTASKPRDHPVQNNPEALKT	180
Db		268	TDSGNIDAAKD-----IIRYIIGIKGHFQTKESQETLHKPASKPASEGFVKILDTPEKLKD	322
QY		181	IQNQLREXX	189
Db		323	LFTELOKKI	331

RESULT 6
I56126
lymphocyte function-associated molecule-1-alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56126
R:Kaufmann, Y.; Tseng, B.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A:Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit
A:Reference number: I56126; MIMD:91268576; PMID:2051027
A:Accession: I56126
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1163 <RES>
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:G198785; PID:G198786
C:Genetics:
A:Gene: LFA-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
E:315-315/Domains: von Willebrand factor type A repeat homology <VWAI>

RESULT 7
A33809
cartilage matrix protein precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33809; A26364
R:Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argu
J. Biol. Chem. 264, 8126-8134, 1989
A:Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
grins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A:Reference number: A33809; MUID:89255246; PMID:2542265
A:Accession: A33809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <KIS>
A:Cross-references: UNIPROT:P05099; GR:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235

R:Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A>Title: Structural features of cartilage matrix protein deduced from cDNA.
A:Reference number: A26364; MUID:87092429; PMID:3025875
A:Accession: A26364
A:Molecule type: mRNA
A:Residues: 78-493 <ARG>
A:Cross-references: GB:MI4792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
F:37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VWA2>

RESULT 8

S66522
cartilage matrix protein precursor - mouse

C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522

R/Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996

A/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c

A/Reference number: S66522; MUID:96270751; PMID:8665920

A/Accession: S66522

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-500 <ASZ>

A/Cross-references: UNIPROT:P51942; EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163178

C/Genetics:

A/Gene: CMP

C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-500/Product: cartilage matrix protein #status predicted <MAT>

F/43-210/Domain: von Willebrand factor type A repeat homology <VWA1>

F/231-266/Domain: EGF homology <EGF>

F/227-441/Domain: von Willebrand factor type A repeat homology <VWA2>

F:1756-1838/Domain: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domain: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3Q>
F:2207-2294/Domain: fibronectin type III repeat homology <FN3R>
F:2325-2490/Domain: von Willebrand factor type A repeat homology <VWA4>
F:2438-2440/Region: cell adhesion #status predicted
F:2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F:2899-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F:3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F:32_1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (cov
F:2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #stat

Query Match 22.3%; Score 215; DB 2; Length 3124;
Best Local Similarity 30.6%; Pred. NO. 9.9e-10;
Matches 57; Conservative 37; Mismatches 74; Indels 18; Gaps 4;

QY 6 SDIAFLIDSGSIIPHDFRMKEFVSTWME--QLKKSXTLPSLMQYSEFRHFTFEKQ 63

DB 138 TDLVFDGWSVGNFRYILDFFVALVSAPDIGEEKIRVGVQYSSDTRTFEFLNQYF 197

QY 64 NNPNRSIVKPIITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGERKFGDPL 123

DB 198 RRSLLDALKIPYKGNWNTGEADYLVKNTFTESAGARKGFPKVAIVITDGA----- 252

QY 124 GYEDVIPADRE---GVIRYVIGVDAPRSEKSOELNTIASKPPRDHVFQVNNFEALK 179

DB 253 --QDEVEIPARELNRNIGVEVSLGKAA-----DAKELKLIASQPSLKHVFNVANFDGIV 305

QY 180 TIONQL 185

DB 306 DIONEI 311

RESULT 11

A45974

collagen alpha 1(XIV) chain precursor, short form 2 - chicken

N:Alternate names: undulin

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A45974; S30085; S22916; S17035; S20833

R:Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin

J. Biol. Chem. 268, 12177-12184, 1993

A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region

ns.

A:Reference number: A45974; MUID:93280195; PMID:8505337

A:Accession: A45974

A:Status: preliminary

A:Molecule type: mRNA, protein

A:Residues: 1-1747 <GER>

A:Cross-references: UNIPROT:P32018

A:Experimental source: embryo skin

A>Note: sequence inconsistent with the nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBI:133364, NCBI:133365)

R:Apfe, S.S.

submitted to the EMBL Data Library, March 1992

A:Reference number: S30085

A:Accession: S30085

A:Molecule type: mRNA

A:Residues: 1472-1660 <APT>

A:Cross-references: EMBL:X65122; NID:962871; PIDN:CAA46238.1; PID:9938175

R:Trueb, J.; Trueb, B.

Eur. J. Biochem. 207, 549-557, 1992

A:Title: Type XIV collagen is a variant of undulin.

A:Reference number: S22916; MUID:92339443; PMID:1339349

A:Accession: S22916

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>

R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linenmayer, T.F.; van der Rest, M.; Mayne, F.
Eur. J. Biochem. 201, 333-338, 1991

A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens v

A:Reference number: S17035; MUID:92037585; PMID:1935930

A:Accession: S17035

A:Molecule type: mRNA

A:Residues: 1472-1659 <GOR1>

A:Accession: S20833

A:Molecule type: protein

A:Residues: 1551-1570/1593-1599,1639-1667 <GOR2>

C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimmer

F:40-204/Domain: von Willebrand factor type A repeat homology <VWA1>

F:236-317/Domain: fibronectin type III repeat homology <FN3A>

F:326-409/Domain: fibronectin type III repeat homology <FN3B>

F:418-498/Domain: fibronectin type III repeat homology <FN3C>

F:507-591/Domain: fibronectin type III repeat homology <FN3D>

F:625-707/Domain: fibronectin type III repeat homology <FN3E>

F:716-798/Domain: fibronectin type III repeat homology <FN3F>

F:806-893/Domain: fibronectin type III repeat homology <FN3G>

F:924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>

F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>

F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>

F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 22.2%; Score 214.5; DB 2; Length 1747;

Best Local Similarity 32.4%; Pred. NO. 5.3e-10;

Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPQEDSDTAFILDGSGSIIPHDFRMKEFV-STV--MEQLKSKTLPFLSMQYSEFRHFT 57

DB 920 CKAARADLVFLVDGWSIGDDNFNKKIISFLYSTVGVGALDKIGDPGVQVAIQFSDDPRTF 979

QY 58 TFKFQNNPNRSIVKPIITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGE 117

DB 980 KLNAYKTKETLEALQIAYKGNTKGKAKHAREVLTGTGAGRKGIKPKVLVITDGR 1039

QY 118 KFGDPLGYEDVIPADREGVIRYVIGVDAPRSEKSOELNTIASKPPRDHVFQVNNFEA 177

DB 1040 SQDD---VNKVSREMQLDGFSAIGVADADYS-----ELVNIGSKPSERHVFVDDFDA 1091

QY 178 LKTIONQL 185

DB 1092 FTKIEDEL 1099

RESULT 12

S31212

collagen alpha 1(XIV) chain precursor, short form - chicken

C:Species: Gallus gallus (chicken)

C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003

C:Accession: S31212

R:Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.

Eur. J. Biochem. 212, 483-490, 1993

A:Title: Complete primary structure of chicken collagen XIV.

A:Reference number: S31211; MUID:93185668; PMID:8444186

A:Accession: S31212

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-1857 <WAE>

A:Cross-references: EMBL:X70792; NID:928874; PIDN:CAA50063.1; PID:9288875

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C:Genetics:

A:Gene: Col14A1

C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimmer

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <WAT>

F:129-110/Domain: fibronectin type III repeat homology <FN3A>

F:156-320/Domain: von Willebrand factor type A repeat homology <VWA1>

F:352-433/Domain: fibronectin type III repeat homology <FN3B>

F:442-525/Domain: fibronectin type III repeat homology <FN3C>

F:534-614/Domain: fibronectin type III repeat homology <FN3D>

F:623-707/Domain: fibronectin type III repeat homology <FN3E>

F:741-823/Domain: fibronectin type III repeat homology <FN3F>

F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 22.2%; Score 214.5; DB 2; Length 1857;
Best Local Similarity 32.4%; Pred. No. 5.7e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;
QY 1 CPQEDSDIAFLDGGSGIIPHDPRRMKEFV-STV--MEQLKSKTLFSLMYSSEFRHIF 57
DB 1036 CRAAKADLVFLVDGWSIGDDNFNKIISFLYSTVGALDKIGDPGTQVAIIQFSDDPRTF 1095
QY 58 TFKEFQNNPRLSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGE 117
DB 1096 KLNAYKTETLEAIIQAIYKGGNTKTGKAIKHAREVLFTGEAGMRKGIPKVLVITDGR 1155
QY 118 KFGDPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEA 177
DB 1156 SQDD---VNKVSREMQLDGFSSFAIGVADADYS-----ELVNIGSKPSERHVFVDVDDFA 1207
QY 178 LKTIONQL 185
DB 1208 FTKIEDEL 1215
RESULT 13
S78476
collagen alpha 1(XIV) chain precursor, long form - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S78476; S31211
R:Trueb, B.
submitted to the EMBL Data Library, January 1993
A:Reference number: S78476
A:Accession: S78476
A:Molecule type: mRNA
A:Residues: 1-1888 <TR>
A:Cross-references: UNIPROT:P32018; EMBL:X70793; PID:G288872; PIDN:CAA50064.1; PID:G2888
R:Waelechi, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:8444186
A:Accession: S31211
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416; 1460-1811, 1843-1888 <WAE>
A:Cross-references: EMBL:X70793
C:Genetics:
A:Gene: Coll4A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>
F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 22.2%; Score 214.5; DB 2; Length 1888;
Best Local Similarity 32.4%; Pred. No. 5.8e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;
QY 1 CPQEDSDIAFLDGGSGIIPHDPRRMKEFV-STV--MEQLKSKTLFSLMYSSEFRHIF 57
DB 1036 CRAAKADLVFLVDGWSIGDDNFNKIISFLYSTVGALDKIGDPGTQVAIIQFSDDPRTF 1095
QY 58 TFKEFQNNPRLSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGE 117

DB 1096 KLNAYKTETLEAIIQAIYKGGNTKTGKAIKHAREVLFTGEAGMRKGIPKVLVITDGR 1155
QY 118 KFGDPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEA 177
DB 1156 SQDD---VNKVSREMQLDGFSSFAIGVADADYS-----ELVNIGSKPSERHVFVDVDDFA 1207
QY 178 LKTIONQL 185
DB 1208 FTKIEDEL 1215
RESULT 14
A45226
integrin alpha-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45226
R:Bricegowitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A:Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
A:Reference number: A45226; MUID:93155124; PMID:8428973
A:Accession: A45226
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1151 <BRI>
A:Cross-references: UNIPROT:P56199
A:Experimental source: hepatoblastoma cell line HepG2
A:Note: sequence extracted from NCBI backbone (NCBI:P124326)
F:142-317/Domain: von Willebrand factor type A repeat homology <VWA1>
Query Match 21.5%; Score 207.5; DB 2; Length 1151;
Best Local Similarity 29.8%; Pred. No. 1.2e-09;
Matches 57; Conservative 39; Mismatches 84; Indels 11; Gaps 5;
QY 7 DIAFLDGGSGIIPHDPRRMKEFVSTVMEQLK--KSKTLFSLMYSSEFRHIFTPKEFQN 64
DB 144 DIVILDGNSIYPWD--SVTAFDLNLLKRMIDGPKQTQVGIVQGENVTHEFNLMKYS 201
QY 65 NPNRSLVKPITQLGR--THATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
DB 202 TEEVLVAKKIVQGRGRTMTALGTDTARKEAFTGARRGVKKVMVITDGESH-DNH 260
QY 124 GYEDVIPADREGVIRYVIGVGDAFR-----SEKSRQELNTIASKPPRDHVFQVNNFEAL 178
DB 261 RLKVIQDCEDENIQRFSAIILGYNRGNLSTEFKEIKSIASEPTKHFNFVSDDEL 320
QY 179 KTIQNLREKX 189
DB 321 VTIVTLGERI 331
RESULT 15
S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C:Accession: S42373
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-3051 <SMI>
A:Cross-references: EMBL:Z30423; NID:G458479; PID:G458485
C:Genetics:
A:Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
F:512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F:754-793/Domain: fibronectin type II repeat homology <2F1>
F:1201-1244/Domain: EGF homology <EGF>
Query Match 21.5%; Score 207.5; DB 2; Length 3051;
Best Local Similarity 31.5%; Pred. No. 4.2e-09;
Matches 63; Conservative 41; Mismatches 71; Indels 25; Gaps 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 39.5668 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-B_COPY_144_332

Perfect score: 966

Sequence: 1 CPQSDSDIAFLIDSGSIIP.....FQVNNFEALTIQNLREKX 189

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	1152	1	ITAM_HUMAN
2	778	80.5	920	2	Q28984
3	746	77.2	1153	1	ITAM_MOUSE
4	719	74.4	1151	2	Q9J130
5	595	61.6	1161	1	ITAD_RAT
6	586	60.7	1162	1	ITAD_HUMAN
7	583	60.4	205	2	Q63001
8	540	55.9	1163	1	ITAX_HUMAN
9	534	55.3	1188	2	Q6KAS4
10	534	55.3	1188	2	BAD21383
11	533	55.2	1169	1	ITAX_MOUSE
12	408	42.2	304	2	Q6PG66
13	408	42.2	304	2	AAH57200
14	344	35.6	895	2	Q9WUF8
15	344	35.6	1167	2	Q88340
16	341	35.3	1038	2	Q8BS01
17	338	35.0	1167	1	ITAX_MOUSE
18	328	34.0	1179	1	ITAE_HUMAN
19	327	33.9	1160	2	Q8MKF4
20	323.5	33.5	1167	2	Q88341
21	319	33.0	231	2	Q8N882
22	294	30.4	79	2	Q8HY27
23	294	30.4	79	2	Q8HY41
24	291.5	30.2	1170	1	ITAL_HUMAN
25	284.5	29.5	1165	1	ITAL_BOVIN
26	275	28.5	269	2	Q8OWE9
27	264.5	27.4	1196	2	Q9RTF1
28	261	27.0	1160	2	Q9R200
29	261	27.0	1161	2	Q9WTV4
30	261	27.0	1163	1	ITAL_MOUSE
31	260.5	27.0	1166	2	Q6TYB8

32	260.5	27.0	1166	2	AAQ90015	AAQ90015 bos taurus
33	250.5	25.9	1187	2	Q98TF0	Q98TF0 cyprinus ca
34	242	25.1	493	1	CAMA_CHICK	P05099 gallus gall
35	238	24.6	257	2	Q8C270	Q8C270 mus musculus
36	237	24.5	652	2	Q95LI2	Q95LI2 bos taurus
37	235	24.3	500	1	CAMA_MOUSE	P51942 mus musculus
38	235	24.3	500	2	Q8OVN5	Q8OVN5 mus musculus
39	232	24.0	496	1	CAMA_HUMAN	P21941 homo sapien
40	231	23.9	656	2	Q96DT1	Q96DT1 homo sapien
41	231	23.9	678	2	Q9UDN0	Q9UDN0 homo sapien
42	231	23.9	678	2	AAQ88704	AAQ88704 homo sapi
43	231	23.9	693	2	Q96DM8	Q96DM8 homo sapien
44	225.5	23.3	1086	2	Q96HB1	Q96HB1 homo sapien
45	223.5	23.1	956	2	Q99K64	Q99K64 mus musculus

ALIGNMENTS

RESULT 1

ID	ITAM_HUMAN	STANDARD;	PRT;	1152 AA.
AC	P11215;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI)			
DE	(Neutrophil adherence receptor).			
CN	Name=ITGAM; Synonyms=CR3A, CD11B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88315033; PubMed=2457584;			
RA	Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;			
RT	"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins von Willebrand factor and factor B.";			
RL	J. Biol. Chem. 263:12403-12411(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88190151; PubMed=2833753;			
RA	Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;			
RT	"Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: Chromosomal localization and homology to the alpha subunits of integrins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88257215; PubMed=2454931;			
RA	Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;			
RT	"Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";			
RL	J. Cell Biol. 106:2153-2158(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93123748; PubMed=8419480;			
RA	Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;			
RT	"Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";			
RL	J. Immunol. 150:480-490(1993).			
RN	[5]			
RP	SEQUENCE OF 9-1153 FROM N.A.			
RX	MEDLINE=89098993; PubMed=2563162;			
RA	Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;			
RT	"cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";			


```
FT SIGNAL 1 16 Integrin alpha-M.
FT CHAIN 17 1152

Query Match
Best Local Similarity 100.0%; Score 966; DB 1; Length 1152;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKSKTLPFSLMOYSEFRHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKSKTLPFSLMOYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDGAFSEKSRQELNTIASKPRDRHVQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDGAFSEKSRQELNTIASKPRDRHVQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
Q28984
ID Q28984 PRELIMINARY; PRT; 920 AA.
AC Q28984;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CD11b (Fragment).
GN Name=CD11b;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.-K., Schook L.B., Rutherford M.S.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; U04072; AAB16869.1; -
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; WVF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; WVA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; WVFADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; WVA; 1.
DR PROSITE; PS0234; WVFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 920
FT SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;

Query Match
Best Local Similarity 80.4%; Score 778; DB 2; Length 920;
Matches 152; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKSKTLPFSLMOYSEFRHFTFK 60
DB 11 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKSKTLPFSLMOYSEFRHFTFK 70
QY 61 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 71 DFKRNPGLLVKPIPTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 130
QY 121 DPLGYEDVPEADREGVIRYVIGVDGAFSEKSRQELNTIASKPRDRHVQVNNFEALKT 180
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DB 131 DPLGYEDVPEADREGVIRYVIGVDGAFNSWKSREELNTIASKPCGDHFVQVNNFEAVKT 190
QY 181 IQNQLREKX 189
DB 191 IQNQLQEXT 199

RESULT 3
ITAM MOUSE
ID ITAM MOUSE STANDARD; PRT; 1153 AA.
AC P05555; Q8CA73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name=Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=86312584; PubMed=3044779;
RA Pyteia R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
RL EMBL J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Ciothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Frazier K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kohno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 11-45 FROM N.A.
RX STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=86287312; PubMed=2942940;
RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
RA Larson R.S., Roberts T.M., Springer T.A.;
RT "A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
RN [4]
```

SEQUENCE OF 17-28.
 MEDLINE=85188276; PubMed=3887182;
 RA Springer T.A., Teplow D.B., Dreyer W.J.;
 RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
 glycoproteins and unexpected relation to leukocyte interferon.";
 RL Nature 314:540-542(1985).
 CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
 adhesive interactions of monocytes, macrophages and granulocytes
 as well as in mediating the uptake of complement-coated particles.
 It is identical with CR-3, the receptor for the iC3b fragment of
 the third complement component. It probably recognizes the R-G-D
 peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
 fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
 of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
 mast cell development and in immune complex-mediated
 glomerulonephritis. Mice expressing a null mutation of the alpha-M
 subunit gene demonstrate increase in neutrophil accumulation, in
 response to a impaired degranulation and phagocytosis, events that
 apparently accelerate apoptosis in neutrophils. These mice develop
 obesity.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
 associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P05555-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P05555-2; Sequence=VSP_010473;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
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 or send an email to license@isb-sib.ch).

 DR EMBL; X07640; CAA30479.1; -;
 DR EMBL; AK039444; BAC30350.1; -;
 DR EMBL; M14293; AAA39484.1; -;
 DR PIR; S00551; S00551.
 DR HSSP; P11215; 1BHO.
 DR MGD; MGI:96607; Itgam.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0007155; P:cell adhesion; IMP.
 DR GO; GO:0045123; P:cellular extravasation; IMP.
 DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS50234; VWFA; 1.
 KW Alternative splicing; Calcium; Cell adhesion;
 KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 1153 Integrin alpha-M.
 FT DOMAIN 17 1105 Extracellular (Potential).

FT	TRANSMEM	1106	1129	POTENTIAL
FT DOMAIN	1130	1153		Cytoplasmic (Potential).
FT REPEAT	31	84		FG-GAP 1.
FT REPEAT	85	163		FG-GAP 2.
FT DOMAIN	164	350		VWFA.
FT REPEAT	337	400		FG-GAP 3.
FT REPEAT	401	452		FG-GAP 4.
FT REPEAT	454	515		FG-GAP 5.
FT REPEAT	517	575		FG-GAP 6.
FT REPEAT	580	632		FG-GAP 7.
FT CA_BIND	465	473		Potential.
FT CA_BIND	529	537		Potential.
FT CA_BIND	592	600		Potential.
FT SITE	1132	1136		GFPR motif.
FT DISULFID	66	73		By similarity.
FT DISULFID	105	123		By similarity.
FT DISULFID	654	711		By similarity.
FT DISULFID	770	776		By similarity.
FT DISULFID	999	1023		By similarity.
FT DISULFID	1028	1033		By similarity.
FT CARBOHYD	58	58		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	86	86		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	391	391		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	696	696		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	734	734		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	772	772		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	801	801		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	881	881		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	907	907		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	941	941		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	980	980		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	994	994		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1022	1022		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1045	1045		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1051	1051		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1076	1076		N-linked (GlcNAc. .) (Potential).
FT VARSPLIC	453	569		Missing (in isoform 2). /FTId=VSP_010473.
FT CONFLICT	37	37		N -> S (in Ref. 2).
FT CONFLICT	683	683		V -> G (in Ref. 2).
SEQ SEQUENCE	1153 AA;	127480 MW;	178DB988ASECB0343 CRC64;	
Query Match	77.2%;	Score 746;	DB 1; Length 1153;	
Best Local Similarity	77.8%;	Pred. No. 7.6e-52;		
Matches 147;	Conservative 20;	Mismatches 22;	Indels 0; Gaps 0;	
QY 1	CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTILFSLMOYSSEERHETFK	60		
DB 144	CPQESDIVLIDGSGSINNIDFQRMKEFVSTVMEQFKSKTILFSLMOYSDEFRIHFTFN	203		
QY 61	EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120		
DB 204	DFKENPSRSHVSPKQLNGTKTAGIRKVVRELFHKTNGARENAKILVITDGEKFG	263		
QY 121	DPLGYEDVIPADREGVIRYVIGVDAPFRSKSQELNTIASKPPRDHVFQNNFEALKT	180		
DB 264	DPLDYKDVIPADRAGVIRYVIGVGNFKNPQSRRELDITASKPAGEHVQVDNFEALNT	323		
QY 181	IONQLREKX	189		
DB 324	IONQLQEKI	332		
RESULT 4				
Q9J130	PRELIMINARY;			
ID Q9J130				
AC Q9J130				
DT 01-OCT-2000	(TrEMBLrel. 15, Created)			
DT 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Integrin beta 2 alpha subunit.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Pathallah D.M. Sr., Zerria K. Jr.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF268593; AAF81280.1; -.
DR HSP; P11215; IBHQ.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; P11185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWF A.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;

Query Match 74.4%; Score 719; DB 2; Length 1151;
Best Local Similarity 74.1%; Pred. No. 1.2e-49;
Matches 140; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDSGSIIPHDFRRMKFVSTVMEQLKSKTLFSLMQYSEEFRIHETPK 60
Db 144 CQQSSNIAFLIDSGSINTIDFQRMKFPVSTVMDQFQSKTLFSLMQYSDERTHTFTN 203
QY 61 EFQNNPRLSKVPTOLLGRHTATGIRKVRRELFNTNGARKNAFKLLVITDGEKFG 120
Db 204 DFKRNPDPKSHVRPIQLNGRTKTASGIRKVRRELFQKINGARDNAAKLVITDGEKFG 263
QY 121 DPLGVEDVTPEDRGVIRYVIGVDAPRSKROELNTIASKPRDHVQVNNFEALKT 180
Db 264 DPLNTEDVTPEDRGVIRYVIGVDAPRSKROELNTIASKPRDHVQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IRNQLQEKI 332

RESULT 5
ID ITAD RAT STANDARD; PRT; 1161 AA.
AC Q9QVE7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.W., VanderVieren M., Kilgannon P.D., Dietsch G.,
RA Gallatin W.M.;
RL "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
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Db 146 CPEQMDIAFLIDSGSINORDPAQMKDFVKALMGFASTSTFLSLMQYNSILKTHFTPT 205
Qy 61 EFQNNPNSLVKPIITOLLGRHTATGIRKVVRELENTNGARKNAFKILVITDGEKFG 120
Db 206 EFKNIIDPQSLVDPIVOLQGLTYTAGIRVMEELFHSKNGSRKSAKILLVITDQKYR 265
Qy 121 DPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 266 DPLEYSDVIPAADKAGIIRYALGVGDFAQEPYALKELNTIGSAPPQDHVFKVGNFALRS 325
Qy 181 IQNLREKX 189
Db 326 IQRLQOEKI 334
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RESULT 6.

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ITAD_HUMAN
ID ITAD_HUMAN STANDARD; PRT; 1162 AA.
AC Q13349; Q15575; Q15576;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor (leukointegrin alpha D) (CD11d) (ADB2).
GN Name=ITGAD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96111956; PubMed=8777714;
RA Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
RT 3.";
RL Immunity 3:683-690(1995).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RX MEDLINE=20187620; PubMed=10722744;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin
RT gene CD11d. Essential role of Sp1 and Sp3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=96257236; PubMed=8666289;
RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene encoding a human
RT beta 2-integrin alpha subunit.";
RL Gene 171:291-294(1996).
RN [4]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
RA Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alpha2beta2 integrin is expressed on human eosinophils and functions
RT as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
RT 1).";
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
RA Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
RT binding interface between I domain and VCAM-1.";
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
```

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CC from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
CC lines and subsets of peripheral blood leukocytes and strongly on
CC tissue-specialized cells, including macrophages foam cells within
CC atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -----
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CC -----
CC EMBL; U37028; AAB38547.1; -
CC EMBL; U40274; AAB60634.1; -
CC EMBL; U40275; AAB60635.1; -
CC EMBL; U40276; AAB60636.1; -
CC EMBL; U40277; AAB60637.1; -
CC EMBL; U40279; AAB60638.1; -
CC EMBL; U40278; AAB60638.1; JOINED.
CC EMBL; AF187881; AAF62875.1; -
CC HSSP; P11215; 1BHQ.
CC Genew; HGNC:6146; ITGAD.
CC MIM; 602453; -
CC GO; GO:0008305; C:integrin complex; TAS.
CC GO; GO:0016337; P:cell-cell adhesion; NAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR000413; Integrin_alpha.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF01839; FG-GAP; 3.
CC Pfam; PF00357; Integrin_alpha; 1.
CC Pfam; PF00092; VWA; 1.
CC PRINTS; PR01185; INTEGRINA.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00191; Int_alpha; 5.
CC SMART; SM00327; VWA_1.
CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE; PS50234; VWFA; 1.
CC Kew Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 1162 Integrin alpha-D.
FT DOMAIN 18 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1162 Cytoplasmic (Potential).
FT REPEAT 32 85 FG-GAP 1.
FT REPEAT 86 ? FG-GAP 2.
FT REPEAT 150 332 VWFA.
FT DOMAIN 350 400 FG-GAP 3.
FT REPEAT 401 452 FG-GAP 4.
FT REPEAT 454 516 FG-GAP 5.
FT REPEAT 518 576 FG-GAP 6.
FT REPEAT 581 633 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 530 538 Potential.
FT CA_BIND 593 601 Potential.
FT SITE 1127 1131 GFFKR motif.
FT DISULFID 67 74 By similarity.
FT DISULFID 106 124 By similarity.
FT DISULFID 655 710 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 846 861 By similarity.
FT DISULFID 994 1018 By similarity.
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FT	DISULFID	1023	1028	By similarity.
FT	CARBOHYD	59	59	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	87	87	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	99	99	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	391	391	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	691	691	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	733	733	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	873	873	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	957	957	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1046	1046	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	500	500	Missing (in Ref. 2).
FT	CONFLICT	515	518	CHPW -> ATP (in Ref. 2).
FT	CONFLICT	825	825	L -> V (in Ref. 2).
FT	CONFLICT	984	984	L -> V (in Ref. 2).
SQ	SEQUENCE	1162 AA; 126885 MW; F296A1A35455D77D	CRC64;	
Query Match				
Best Local Similarity 60.7%; Score 586; DB 1; Length 1162;				
Matches 114; Conservative 32; Mismatches 43; Indels 0; Gaps 0;				
QY	1	CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMQYSEBFRIFHTPK	60	
Db	144	CPHQEMDIVFLIDGSGSIDQNDFNQMKGFQAVMGQFEGTDTLFLALMQYSLNLKIHFTPT	203	
QY	61	EQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG	120	
Db	204	QFRTSPSQSLVDPIVQLKGLTFTATGILTVVTLFHHKNGARKSAKKILVITDQGYK	263	
QY	121	DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQSLNTIASKPPDRHVFQVNNFEALKT	180	
Db	264	DPLESDVIVPQAEKAGIIRYAGVHAFOGPTARQELNTISSAPPQDHVFKVDNFAALGS	323	
QY	181	IQNLREKX	189	
Db	324	IQQLQEKI	332	
RESULT 7				
Q63001	PRELIMINARY; PRT; 205 AA.			
AC	Q63001;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Integrin alpha-M (Fragment).			
GN	Name=Itgam;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar Kyoto;			
RA	Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,			
RA	Julier C., Masuda J., Yamori Y., Nara Y.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U59801; AAB03226.1; -			
DR	GO; GO:0007229; P.integrin-mediated signaling pathway; IEA.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF00092; VWA; 1.			
DR	PRINTS; PRO0453; VWFADOMAIN.			
DR	SMART; SM00327; VWA; 1.			
DR	PROSITE; PS00234; VWFA; 1.			
KW	Integrin.			
FT	NON_TER	1	1	
FT	NON_TER	205	205	
SQ	SEQUENCE	205 AA; 42292 MW; C8C2D9395008DA36	CRC64;	
Query Match				
Best Local Similarity 60.4%; Score 583; DB 2; Length 205;				
Matches 119; Conservative 17; Mismatches 24; Indels 0; Gaps 0;				
QY	30	VSTVMEQLKSKTLFSLMQYSEBFRIFHTFKBFQNNPNRSLVKPITQLLGRTHATGIR	89	

Db	1	VSTVMEQFQKSKTFLSLMQYSEDFRTHFTFNFKENPDKSHVPIRQLNGRKTASGIR	60
QY	90	KVVRLEFNITWGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVDAPR	149
Db	61	KVVRLEFQKINGARDNAAKILVITDGEKFGDPLGVEDVPEABEAGIIRYVIGVXNAFH	120
QY	150	SEKSRQELNTIASKPPDRDHVFQVNNFEALKTIONQLREKX	189
Db	121	KPQSRRELDTIASKPAGDHVFQVDNFEALNTIRNLQLEKI	160

RESULT 8

ITAX	HUMAN	STANDARD; PRT; 1163 AA.
ID	ITAX	
AC	P20702; O81VA6;	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	05-JUL-2004 (Rel. 44, Last sequence update)	
DT	01-OCT-2004 (Rel. 45, Last annotation update)	
DE	Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95	
DE	alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).	
GN	Name=ITGAX; Synonyms=CD11C;	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=88166645; PubMed=3327687;	
RA	Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;	
RT	"cDNA cloning and complete primary structure of the alpha subunit of a	
RT	leukocyte adhesion glycoprotein, p150,95.;"	
RL	EMBO J. 6:4023-4028(1987).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=90153906; PubMed=2303426;	
RA	Corbi A.L., Garcia-Aguilar J., Springer T.A.;	
RT	"Genomic structure of an integrin alpha subunit, the leukocyte p150,95	
RT	molecule.;"	
RL	J. Biol. Chem. 265:2782-2788(1990).	
RN	[3]	
RP	ERRATUM.	
RA	Corbi A.L., Garcia-Aguilar J., Springer T.A.;	
RL	J. Biol. Chem. 265:12750-12751(1990).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.;"	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[5]	
RP	SEQUENCE OF 20-43.	
RX	MEDLINE=87167596; PubMed=3549901;	
RA	Miller L.J., Wiebe M., Springer T.A.;	
RT	"Purification and alpha subunit N-terminal sequences of human Mac-1	

RT and p150,95 leukocyte adhesion proteins." ;
 RL J. Immunol. 138:2381-2383(1987).
 CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
 CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
 CC interaction during inflammatory responses. It is especially
 CC important in monocyte adhesion and chemotaxis.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11c.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M81695; AA559180.1; -;
 DR EMBL; M29165; -; NOT ANNOTATED CDS.
 DR EMBL; M29487; AA51620.1; ALT SEQ.
 DR EMBL; M29482; AA51620.1; JOINED.
 DR EMBL; M29483; AA51620.1; JOINED.
 DR EMBL; M29484; AA51620.1; JOINED.
 DR EMBL; M29485; AA51620.1; JOINED.
 DR EMBL; M29486; AA51620.1; JOINED.
 DR EMBL; BC038237; AAH38237.1; -;
 DR PIR; A36584; RWHUIC.
 DR PDB; 1N3V; X-ray; A=141-338.
 DR Genem; HGNC:6152; ITGAX.
 DR MIM; 151510; -;
 DR GO; GO:0008305; C:integrin complex; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0009887; P:organogenesis; TAS.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR02035; VWF_A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS0234; VWFA; 1.
 DR 3d-structure; Calcium; Cell adhesion; Direct protein sequencing;
 KW Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 1163
 FT DOMAIN 20 1107
 FT TRANSMEM 1108 1128
 FT DOMAIN 1129 1163
 FT REPEAT 34 87
 FT REPEAT 88 ?
 FT DOMAIN 165 351
 FT REPEAT ? 401
 FT REPEAT 402 453
 FT REPEAT 455 517
 FT REPEAT 518 576
 FT REPEAT 581 633
 FT CA_BIND 466 474
 FT CA_BIND 530 538
 Integrin alpha-X.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 FG-GAP 1.
 FG-GAP 2.
 VWFA.
 FG-GAP 3.
 FG-GAP 4.
 FG-GAP 5.
 FG-GAP 6.
 FG-GAP 7.
 Potential.

CA_BIND 593 601
 SITE 1131 1135
 DISULFID 169 176
 DISULFID 108 126
 DISULFID 655 712
 DISULFID 771 777
 DISULFID 848 863
 DISULFID 998 1022
 DISULFID 1027 1032
 CARBOHYD 61 61
 CARBOHYD 89 89
 CARBOHYD 392 392
 CARBOHYD 697 697
 CARBOHYD 735 735
 CARBOHYD 899 899
 CARBOHYD 939 939
 CARBOHYD 1050 1050
 VARIANT 48 48
 CONFLICT 209 209
 CONFLICT 251 251
 CONFLICT 469 469
 CONFLICT 490 490
 CONFLICT 547 547
 CONFLICT 756 756
 CONFLICT 819 819
 CONFLICT 1161 1163
 STRAND 150 157
 TURN 160 161
 HELIX 164 178
 TURN 179 180
 TURN 183 185
 STRAND 186 193
 STRAND 197 201
 HELIX 203 208
 HELIX 212 216
 TURN 217 218
 STRAND 226 226
 HELIX 228 236
 TURN 237 240
 HELIX 242 244
 TURN 245 245
 TURN 248 249
 STRAND 251 258
 STRAND 263 263
 HELIX 269 278
 TURN 279 280
 STRAND 282 288
 TURN 290 293
 TURN 296 297
 HELIX 298 304
 HELIX 310 312
 STRAND 313 316
 HELIX 319 325
 TURN 326 334
 TURN 335 335
 SQ SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DE8F CRC64;
 Query Match 55.9%; Score 540; DB 1; Length 1163;
 Best Local Similarity 55.6%; Pred. No. 4,2e-35;
 Matches 105; Conservative 35; Mismatches 49; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDSGSIIPHDFFRMKEFVSTVMEQLKSKTSLFSLMOYSEEFRIHFTFK 60
 DB 145 CPRQEDIVFLIDSGSISSENFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQHTFTFE 204
 QY 61 EFQNNPNRSLVKPITOLLGTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 DB 205 EFRRTSNPLSLASVHQLOQGYTTATLQNVHRLFHASYGARRDATKILVITDCKEKG 264
 QY 121 DPLGYEDVPEADREGVIRYVIGGDADFRRSEKSRQELNTIASKPPRDHVFQVNNFEALK 180
 DB 265 DSLDYKDVIPWADAAGIIRYAIGVGLAFQNNRNWELNDIASKPSQEHIFKVEDFDALDK 324

QY 181 IQNQLREKX 189
 DB 325 IQNQLKEKI 333
 RESULT 9
 Q6KAS4
 ID Q6KAS4 PRELIMINARY; PRT; 1188 AA.
 AC Q6KAS4
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE MFLJ00114 protein (Fragment).
 GN MFLJ00114
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.,
 RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene:
 RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
 RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK131133; BAD21383.1; --
 FT NON_TER 1
 SQ SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
 RP
 Query Match 55.3%; Score 534; DB 2; Length 1188;
 Best Local Similarity 54.5%; Pred. No. 1.3e-34;
 Matches 103; Conservative 33; Mismatches 53; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 DB 165 CPKQDQDIVFLIDGSGSISSTDFEKMLDFVKAVMSQLQRPSTFSLMQFSDFYRVHFTFN 224
 QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
 DB 225 NFISTSPSLSDSVRQLRGYTTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 284
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 285 DNLSYDSVIPMAEAAASIRYAIGVGKAFYNEHSKQELKAIASMSHSEYVSVENFDALKD 344
 QY 181 IQNQLREKX 189
 DB 345 IENQLKEKI 353
 RESULT 11
 ITAX MOUSE
 ID ITAX MOUSE STANDARD; PRT; 1169 AA.
 AC Q9QXH4;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
 DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
 GN Name=ItgaX;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dendritic cell;
 RA Huang X., Gorski K., Tong C., Rattis F.-M., Teeng S.-Y., Pardoll D.,
 RA Tsuchiya H.;
 RT "Isolation of genes selectively expressed by dendritic cells.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
 CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
 CC interaction during inflammatory responses. It is especially
 CC important in monocyte adhesion and chemotaxis (By similarity).
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
 CC associates with beta-2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)

```

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Integrin alpha E1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98056820; PubMed=9394838;
RA Brenan M., Rees D.J.G.;
RT "Sequence analysis of rat integrin alpha E1 and alpha E2 subunits:
RT tissue expression reveals phenotypic similarities between
RT intraepithelial lymphocytes and dendritic cells in lymph."
RL Eur. J. Immunol. 27:3070-3079(1997).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF020045; AAC23662.1; -.
DR HSSP; P11215; IBHQ.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1167 AA; 128969 MW; D88A2C38ACDC2AAE CRC64;

Query Match      35.6%; Score 344; DB 2; Length 1167;
Best Local Similarity 37.6%; Pred. No. 3.6e-19;
Matches 71; Conservative 47; Mismatches 69; Indels 2; Gaps 1;

QY 3 QEDSDIAFLIDGSGSIIPHDPRRMEFVSTVMEQL--KSKTLFSLMOYSEEFRIHETFK 60
Db 191 EDGETAIVLDGSGSIEPSDFQKAKNFISTMRNFYEKFCFCNPAIVQYGAIVQTEFDLQ 250

QY 61 EFQNNPNRSLVKPTQLLGRTHRTATGIRKVVRELFTNITNGARKNAFKILVVTGDKFG 120
Db 251 ESRDINASLAKVQSIQVQKVEVTKTASAMQHVLNDNIFIPSGSRKKALKVMVLTGDIQ 310

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 311 DPLNLTTVINSPKMQGVVRFAGVGFADPKNNNTYELKLIASDPKKAHTFKVTNYSALDG 370

QY 181 IQQLREKX 189
Db 371 LLSKLQRI 379

```

Search completed: January 13, 2005, 15:18:43
Job time : 40.5668 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 14:59:41 ; Search time 35.3364 Seconds
(without alignments)
1918.696 Million cell updates/sec

Title: RWHULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLDGGSIIP.....FQVNNFEALKTQNQLREKX 189
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	1152	8	ADM99589 Human int
2	966	100.0	1152	8	ADP12435 Protein e
3	966	100.0	1153	2	AAR04136 Alpha sub
4	966	100.0	1153	2	Aaw65090 Human Bet
5	966	100.0	1153	3	Aab07360 Human CD1
6	966	100.0	1153	5	Aau80252 Human int
7	966	100.0	1153	5	ABG61469 Human Bet
8	966	100.0	1153	5	Aao14428 Integrin
9	966	100.0	1153	7	ADD25615 Binding d
10	960	99.4	187	2	AAY21991 Human com
11	956	99.0	191	5	Aau76856 Human int
12	956	99.0	191	5	Aau76847 Human int
13	934	96.7	216	4	AAB66766 Amino aci
14	934	96.7	435	2	AAR77461 GST-I-dom
15	893	92.4	177	5	Aau76866 Human int
16	890	92.1	177	5	Aau76865 Human int
17	737	76.3	199	5	Abb78072 Murine I-
18	595	61.6	1151	2	Aaw23059 Rat beta
19	595	61.6	1151	2	Aaw60001 Rat alpha
20	595	61.6	1151	2	Aaw65101 Rat beta-
21	595	61.6	1151	2	Aaw72834 Rat alpha
22	595	61.6	1151	2	Aaw73344 Rat alpha
23	595	61.6	1151	3	Aab07371 Rat alpha
24	595	61.6	1151	5	ABG61480 Rat Beta2
25	595	61.6	1161	2	AAR78169 Rat alpha

26	595	61.6	1161	2	AAW23062	Aaw23062 Rat beta
27	595	61.6	1161	2	AAW60004	Aaw60004 Rat alpha
28	595	61.6	1161	2	AAW65104	Aaw65104 Rat beta-
29	595	61.6	1161	2	AAW72824	Aaw72824 Rat alpha
30	595	61.6	1161	2	AAW73345	Aaw73345 Rat alpha
31	595	61.6	1161	3	AAW07374	Aab07374 Rat alpha
32	595	61.6	1161	5	ABG61483	ABG61483 Rat Beta2
33	594	61.5	413	2	AAW23065	Aaw23065 Rabbit be
34	594	61.5	413	2	AAW65107	Aaw65107 Rabbit be
35	594	61.5	413	2	AAW72839	Aaw72839 Rabbit al
36	594	61.5	413	2	AAW73348	Aaw73348 Rabbit al
37	594	61.5	413	3	AAW07377	Aab07377 Rabbit al
38	594	61.5	1151	2	AAR78179	Aar78179 Rat alpha
39	592	61.3	413	5	ABG61486	ABG61486 Rabbit Be
40	586	60.7	1155	2	AAR78167	Aar78167 Mouse alp
41	586	60.7	1155	2	AAW23060	Aaw23060 Mouse bet
42	586	60.7	1155	2	AAW60002	Aaw60002 Mouse alp
43	586	60.7	1155	2	AAW65102	Aaw65102 Mouse bet
44	586	60.7	1155	2	AAW72835	Aaw72835 Mouse alp
45	586	60.7	1155	2	AAW73346	Aaw73346 Mouse alp

ALIGNMENTS

RESULT 1
ADM99589
ID ADM99589 standard; protein; 1152 AA.

XX ADM99589;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human integrin alphaM subunit precursor protein.
XX
KW integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
KW osteopathic; cytostatic; immunosuppressive; antiinflammatory;
KW neuroprotective; antischlicking; immunotherapy; inflammatory;
KW autoimmune disorder; thrombosis; cancer; osteoporosis;
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
KW alphas.
XX Homo sapiens.

XX
FH Key Location/Qualifiers
FT Misc-difference 965 /note= "Encoded by CCC"
FT

XX WO2004007530-A2.
XX
PD 22-JAN-2004.
XX
PF 17-JUL-2003; 2003WO-US022301.
XX
PR 17-JUL-2002; 2002US-0396783P.
PR 17-JUL-2002; 2002US-0396790P.
PR 11-SEP-2002; 2002US-0410135P.

XX (BLOO-) CENT BLOOD RES INC.
XX
XX Springer TA, Takagi J;
PI WPI; 2004-122877/12.
XX N-PSDB; ADM99588.

XX Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
XX
XX Disclosure; SEQ ID NO 4; 232pp; English.
XX
XX The invention relates to a novel isolated or recombinant modified integrin protein having extracellular domains of integrin alpha and beta

CC subunits where one of the subunits has one or more mutations, an altered
CC surface feature or an amino acid substitution or internal deletion,
CC extracellular domains of the integrin beta subunit that comprise a
CC mutation that alters a non-cysteine residue to cysteine or extracellular
CC domains of integrin alpha and beta subunits. The polypeptide of the
CC invention demonstrates antipneumatic, thrombolytic, anticoagulant,
CC osteopathic, cytostatic, immunosuppressive, antiinflammatory,
CC neuroprotective and anticlumping activities and may be useful for
CC immunotherapy in order to prevent or treat an integrin-mediated disorder
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
CC sclerosis. The current sequence is that of the human integrin alpha
CC subunit precursor protein of the invention.
XX
SQ Sequence 1152 AA;

Query Match 100.0%; Score 966; DB 8; Length 1152;
Best Local Similarity 99.5%; Pred. NO. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
ADP12435
ID ADP12435 standard; protein; 1152 AA.
AC ADP12435;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #45.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 20-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX

PS Claim 65; SEQ ID NO 2444; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC vital, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 1152 AA;

Query Match 100.0%; Score 966; DB 8; Length 1152;
Best Local Similarity 99.5%; Pred. NO. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 3
AAR04136
ID AAR04136 standard; protein; 1153 AA.
AC AAR04136;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 07-SEP-1990 (first entry)
XX
DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
XX
KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
KW non-specific defence system; integrin gene superfamily.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Region 1..16
FT /label= signal_peptide
FT Modified-site 86..88
FT /label= putative N-glycosylation site
FT Modified-site 240..242
FT /label= putative N-glycosylation site
FT Modified-site 391..393
FT /label= putative N-glycosylation site
FT Modified-site 469..471
FT /label= putative N-glycosylation site
FT Modified-site 693..695
FT /label= putative N-glycosylation site
FT Modified-site 697..699
FT /label= putative N-glycosylation site
FT Modified-site 735..737
FT /label= putative N-glycosylation site

FT Modified-site 802..804
 FT /label= putative N-glycosylation site
 FT Modified-site 881..883
 FT /label= putative N-glycosylation site
 FT Modified-site 901..903
 FT /label= putative N-glycosylation site
 FT Modified-site 912..914
 FT /label= putative N-glycosylation site
 FT Modified-site 941..943
 FT /label= putative N-glycosylation site
 FT Modified-site 947..949
 FT /label= putative N-glycosylation site
 FT Modified-site 979..981
 FT /label= putative N-glycosylation site
 FT Modified-site 994..996
 FT /label= putative N-glycosylation site
 FT Modified-site 1022..1024
 FT /label= putative N-glycosylation site
 FT Modified-site 1045..1047
 FT /label= putative N-glycosylation site
 FT Modified-site 1051..1053
 FT /label= putative N-glycosylation site
 FT Modified-site 1076..1078
 FT /label= putative N-glycosylation site
 FT Region 1106..1134
 FT /label= putative_transmembrane_region
 FT
 XX EP364690-A.
 XX
 PN 25-APR-1990.
 XX
 XX
 PD
 XX
 XX 17-AUG-1989; 89EP-00115159.
 PF
 XX 23-AUG-1988; 88US-00235353.
 PR
 XX 09-MAR-1989; 89US-00321239.
 PR
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 XX Springer TA, Corbi A;
 PI
 XX
 XX WPI: 1990-125938/17.
 DR
 XX N-PSDB; AAQ04043.
 DR
 XX
 PT New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating
 PT inflammation and viral infections, and in diagnosis.
 PT
 XX
 PS Disclosure; Page ?; 3pp; English.
 XX
 CC Mac-1 alpha subunit is involved in the response to inflammation, i.e.
 CC recognition of and migration to sites of inflammation. It also attaches
 CC to cellular substrates as part of this function making it useful in
 CC visualising endothelial tissue. Mac-1 is a member of the Integrin Gene
 CC superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
 CC -MAR-2003 to correct PA field.)
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key
 CC and pages
 CC
 XX Sequence 1153 AA;
 SX
 Query Match 100.0%; Score 966; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.5e-96;
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTPK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTPK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKX 189
 DB 324 IQNQLREKI 332
 RESULT 4
 AAW65090
 ID AAW65090 standard; protein; 1153 AA.
 XX
 AC AAW65090;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Human Beta-integrin CD11b subunit protein.
 XX
 KW Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
 KW type-I diabetes; atherosclerosis; multiple sclerosis; asthma;
 KW lung inflammation; acute respiratory distress syndrome; CD11b subunit;
 KW rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US5728533-A.
 XX
 PD 17-MAR-1998.
 XX
 PF 07-JUN-1995; 95US-00485618.
 XX
 PR 23-DEC-1993; 93US-00173497.
 PR 05-AUG-1994; 94US-00286889.
 PR 21-DEC-1994; 94US-00362652.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Van Der Vieren M, Gallatin WM;
 XX
 DR WPI: 1998-206565/18.
 XX
 PT Screening assay for modulators of integrin binding - using immobilised or
 PT labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
 XX
 PS Example 5; Fig 1A-D; 106pp; English.
 XX
 CC This sequence represents a human beta-integrin CD11b subunit which is
 CC used to describe a method for identifying compounds that modulate the
 CC interaction of the beta-integrin alpha-d subunit with a binding partner
 CC of alpha-d which involves contacting an alpha-d polypeptide with an alpha
 CC -d binding partner, one of which is immobilised and the other of which is
 CC labelled, in the presence of a test compound, and determining if the
 CC compound affects binding between the alpha-d polypeptide and alpha-d
 CC binding partner, where the alpha-d polypeptide is alpha-d or its fragment
 CC comprising the cytoplasmic, transmembrane or extracellular domain of
 CC alpha-d. Compounds that modulate alpha-d binding could be used to treat
 CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
 CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
 CC and rheumatoid arthritis
 XX
 SX Sequence 1153 AA;
 Query Match 100.0%; Score 966; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.5e-96;
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTPK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTPK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

CC binding of an integrin to a cognate ligand such as Crohn's disease,
CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,
CC Sjogren's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
CC composition comprising the peptide of the invention is useful for
CC treating an integrin mediated disorder in a subject. The polypeptides
CC and/or active or antigenic fragments are useful as reagents for diagnosis
CC of integrin-mediated disorders. The present sequence represents the human
CC integrin-1 alpha-M protein subunit used to generate the mutant
CC polypeptides of the invention
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 966; DB 5; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHIFPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHIFPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDARSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDARSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 7
ID ABG61469 standard; protein; 1153 AA.
XX ABG61469;
AC ABG61469;
DT 27-AUG-2002 (first entry)
DE Human Beta2 integrin alphaCD11b subunit.
XX Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
XX Homo sapiens.
OS
XX
FN WO200230980-A2.
XX
PD 18-APR-2002.
XX
PF 15-OCT-2001; 2001WO-US032059.
XX
PR 13-OCT-2000; 2000US-00688307.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Van Der Vieren M;
XX
DR WPI; 2002-463260/49.
XX
XX Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
PT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
PT limiting autonomic and sensory dysfunction following spinal cord injury.
XX
PS Example 5; Page 191-194; 270pp; English.

XX The invention relates to promoting locomotor recovery, inhibiting
CC locomotor damage, limiting locomotor impairment, or limiting autonomic
CC and sensory dysfunction following spinal cord injury by administering an
CC anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
CC spinal cord injury victim. The method also involves the use of a ligand
CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
CC vascular cell adhesion molecule). The method is useful for promoting
CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
CC impairment, or limiting autonomic and sensory dysfunction following
CC spinal cord injury. In particular, the spinal cord injury comprises
CC compression of the spinal cord. The antibodies are also useful for
CC reducing inflammation at the site of a central nervous system injury. The
CC specification also details the identification of Beta2 integrin alphas
CC CDNA's and proteins, for use in raising the antibodies. Beta2 integrins
CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
CC colitis, immune complex alveolitis and leukaemia. The present sequence is
CC a Beta2 integrin alpha subunit sequence included for comparison with the
CC Beta2 integrin alphas protein sequences
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 966; DB 5; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHIFPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHIFPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDARSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDARSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 8
ID AAO14428 standard; protein; 1153 AA.
XX AAO14428;
AC AAO14428;
DT 03-MAY-2002 (first entry)
DE Integrin Mac-1 alpha subunit.
XX
XX Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
KW open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.
XX
XX OS
XX Unidentified.
XX
XX WO200204521-A2.
XX
XX 17-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021805.
XX
XX 07-JUL-2000; 2000US-0216600P.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

PA (BLOO-) CENT BLOOD RES.
XX Springer T;
XX WPI; 2002-148167/19.
XX New integrin I domain protein having alteration in at least 2
PT noncontiguous regions and exits in an open conformation, useful for
PT treating, preventing or suppressing inflammatory or immunological
PT disorders.
XX Example 1; Fig 1F; 90pp; English.
PS The invention comprises structurally biased variant integrin inserted (I)
XX domain proteins, wherein the alterations to the protein occur in at least
CC two noncontiguous regions. Specifically the variant integrin I domain
CC proteins are structurally biased to exist in the open conformation,
CC thereby altering the binding ability of the protein. The invention also
CC comprises nucleic acids encoding the variant integrin I domain proteins.
CC The integrin I domain proteins and nucleic acids are useful for treating,
CC preventing or suppressing integrin related inflammatory and immunological
CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain
CC proteins and nucleic acids can also be used for treating: ischaemia/
CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral
CC infection; and cancer. The variant integrin I domain nucleic acids and
CC proteins may be used in gene therapy, as vaccines and to screen for
CC bioactive agents. The present amino acid sequence represents the Mac-1
CC alpha subunit of integrin
XX Sequence 1153 AA;
SQ

Query Match 100.0%; Score 966; DB 5; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHFHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHFHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTINGARKNAFLVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTINGARKNAFLVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 9
ADD25615
ID ADD25615 standard; protein; 1153 AA.
XX
AC ADD25615;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #85.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX

PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX (GENE-) GENE-CRAFT INC.
PA
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
PI WPI; 2003-801317/75.
XX
XX New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 176; 157pp; English.
XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 966; DB 7; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHFHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEFRHFHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTINGARKNAFLVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTINGARKNAFLVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVLPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGVEDVLPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332
RESULT 10
AAU71991
ID AAY21991 standard; protein; 187 AA.
AC AAY21991;
DT 13-SEP-1999 (first entry)
DE Human complement factor MAC-1 vWF domain sequence.
KW Factor B analogue; modified; complement activity; complement factor B;
KW short consensus repeat domain; von Willebrand factor domain; human; C2;
KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
OS Homo sapiens.
XX
XX
XX US928892-A.
XX 27-JUL-1999.
XX 26-JUL-1996; 96US-00687706.
XX 03-JAN-1994; 94US-00177109.
XX (UNIW) UNIV WASHINGTON.
XX Oglesby TJ, Hourcade DE;
XX WPI; 1999-429498/36.
XX Nucleic acids encoding complement protein homologues useful for
XX modulating function of the complement system in the treatment of a
XX variety of immune and autoimmune complex mediated syndromes.
XX
XX Disclosure; Fig 5A-B; 53pp; English.
XX
XX The invention relates to a Factor B analogue that exhibits modified
XX complement activity in vitro. The analogue is generated by substituting a
XX short consensus repeat domain (SCR) or a von Willebrand Factor domain
XX (vWF) of human factor B with a SCR or a vWF from a second protein such as
XX human C2 or CR3. The analogues may be used to regulate the complement
XX system involved in immune and autoimmune responses. Complement activity
XX can account for substantial tissue damage in a wide variety of autoimmune
XX /immune complex mediated syndromes such as lupus erythematosus,
XX rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
XX of the complement system using the analogues is likely to provide a means
XX of therapeutic intervention in these cases. Inhibition of complement may
XX also be favorable in cases that involve tissue damage caused by vascular
XX injury such as myocardial infarction, cerebral vascular accidents or
XX acute shock lung syndrome. In these cases the complement system may
XX contribute to the destruction of partially damaged tissue as in
XX reperfusion injury. In addition, the use of complement analogues with
XX novel target specificities could reduce the activity of tissue damaging
XX proteins at sites of inflammation. Complement inhibition is important in
XX the prevention of xenograft rejection (the inhibition of complement by
XX cell-associated and soluble inhibitors is useful in protecting the
XX transplant from damage caused by activation of endogenous complement. The
XX present sequence represents the vWF domain of human factor MAC-1

XX SQ Sequence 187 AA;
Query Match 99.4%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 8.9e-97; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
QY 121 DPLGVEDVLPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGVEDVLPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLRE 187
DB 181 IQNQLRE 187
RESULT 11
AAU76856
ID AAU76856 standard; protein; 191 AA.
XX AAU76856;
XX
XX 21-MAY-2002 (first entry)
XX Human integrin alpha subunit CD11b variant A domain.
XX
XX Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; retinosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antiinflammatory; vasotropic; antiparasitic; vulnerable; gene therapy;
KW mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 189 /label= Gly, Ala
FT /note= "Wild-type Ile substituted by Gly or Ala"
XX
XX WO200209737-A1.
XX
XX 07-FEB-2002.
XX 31-JUL-2001; 2001WO-US023957.
XX 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaut AM, Li R, Xiong J;
XX WPI; 2002-188687/24.
XX
XX Novel high affinity integrin polypeptide useful for treating restenosis
XX and parasitic diseases, comprises all or part of variant integrin alpha
XX subunit A domain or variant integrin beta subunit A-like domain.
XX Claim 2; Page; 55pp; English.
XX
XX The invention relates to a high affinity integrin polypeptide comprising
XX all or part of a variant integrin alpha subunit A domain or a variant
XX integrin beta subunit A-like domain. The polypeptide, preferably the

CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents a human
CC integrin alpha subunit CD11b variant A domain. Note: This variant
CC sequence is not featured in the specification but has been derived from
CC the wild-type protein shown in AAU76847
XX
SQ Sequence 191 AA;

Query Match 99.0%; Score 956; DB 5; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.5e-96;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVVITDGEKFG 120

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 181 IQNQLREKX 189
DB 181 IQNQLREKX 189

RESULT 12
AAU76847
ID AAU76847 standard; protein; 191 AA.
AC AAU76847;
DT 21-MAY-2002 (first entry)
DE Human integrin alpha subunit CD11b A domain.
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 1. 188
XX /note="This region is specifically claimed"
XX WO200209737-A1.
XX
XX 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
XX

DR WPI; 2002-188687/24.
XX Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
PS Example 2; Fig 5; 55pp; English.
XX
CC The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents the human
CC integrin alpha subunit CD11b A domain
XX
SQ Sequence 191 AA;

Query Match 99.0%; Score 956; DB 5; Length 191;
Best Local Similarity 97.9%; Pred. No. 2.5e-96;
Matches 185; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVVITDGEKFG 120

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 181 IQNQLREKX 189
DB 181 IQNQLREKX 189

RESULT 13
AAB66766
ID AAB66766 standard; protein; 216 AA.
XX
AC AAB66766;
XX
DT 10-APR-2001 (first entry)
DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
XX
KW EST; expressed sequence tag; inclusion body; binding partner;
KW immunoglobulins.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200102588-A2.
XX
XX 11-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-EP006137.
XX
XX 02-JUL-1999; 99EP-00112815.
XX
XX (MORP-) MORPHOSYS AG.
XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:13:36 ; Search time 31.2304 Seconds
(without alignments)
2186.449 Million cell updates/sec

Title: RW HULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....FQVNNFEALKTIONLREKX 189

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	191	10	US-09-805-354-1 Sequence 1, Appli
2	966	100.0	191	11	US-09-758-493-1 Sequence 1, Appli
3	966	100.0	191	14	US-10-144-259-1 Sequence 1, Appli
4	966	100.0	1152	9	US-09-945-265-4 Sequence 4, Appli
5	966	100.0	1153	9	US-09-350-259-3 Sequence 3, Appli
6	966	100.0	1153	10	US-09-902-481A-1 Sequence 1, Appli
7	966	100.0	1153	14	US-09-891-943-3 Sequence 3, Appli
8	966	100.0	1153	14	US-10-144-259-30 Sequence 30, Appli
9	966	100.0	1153	14	US-10-207-655-176 Sequence 176, App
10	957	99.1	1137	10	US-09-902-481A-6 Sequence 6, Appli
11	951	98.4	1137	10	US-09-902-481A-5 Sequence 5, Appli
12	941	97.4	1137	10	US-09-902-481A-4 Sequence 4, Appli
13	940	97.3	1187	15	US-10-346-863-37 Sequence 37, Appli

14	940	97.3	187	16	US-10-615-515-9	Sequence 9, Appli
15	939	97.2	184	15	US-10-346-863-17	Sequence 17, Appl
16	934	96.7	190	15	US-10-346-863-42	Sequence 42, Appl
17	934	96.7	190	15	US-10-346-863-48	Sequence 48, Appl
18	934	96.7	216	10	US-09-795-872-5	Sequence 5, Appli
19	934	96.7	216	16	US-10-662-824-5	Sequence 3, Appli
20	928	96.1	1137	10	US-09-902-481A-3	Sequence 3, Appli
21	737	76.3	199	14	US-10-066-551-11	Sequence 11, Appl
22	737	76.3	199	17	US-10-665-990A-11	Sequence 11, Appl
23	595	61.6	1151	9	US-09-350-259-37	Sequence 37, Appl
24	595	61.6	1151	10	US-09-891-943-37	Sequence 37, Appl
25	595	61.6	1161	9	US-09-350-259-55	Sequence 55, Appl
26	595	61.6	1161	10	US-09-891-943-55	Sequence 55, Appl
27	594	61.5	413	9	US-09-350-259-101	Sequence 101, App
28	594	61.5	413	10	US-09-891-943-101	Sequence 101, App
29	586	60.7	191	10	US-09-805-354-3	Sequence 3, Appli
30	586	60.7	191	11	US-09-758-493-3	Sequence 3, Appli
31	586	60.7	191	14	US-10-144-259-3	Sequence 3, Appli
32	586	60.7	1155	9	US-09-350-259-46	Sequence 46, Appl
33	586	60.7	1155	10	US-09-891-943-46	Sequence 46, Appl
34	586	60.7	1161	9	US-09-350-259-2	Sequence 2, Appli
35	586	60.7	1161	9	US-09-350-259-53	Sequence 53, Appl
36	586	60.7	1161	9	US-09-350-259-99	Sequence 99, Appl
37	586	60.7	1161	10	US-09-891-943-2	Sequence 2, Appli
38	586	60.7	1161	10	US-09-891-943-53	Sequence 53, Appl
39	586	60.7	1161	10	US-09-891-943-99	Sequence 99, Appl
40	542	56.1	1163	9	US-09-350-259-4	Sequence 4, Appli
41	542	56.1	1163	10	US-09-891-943-4	Sequence 4, Appli
42	540	55.9	191	10	US-09-805-354-2	Sequence 2, Appli
43	540	55.9	191	11	US-09-758-493-2	Sequence 2, Appli
44	540	55.9	191	14	US-10-144-259-2	Sequence 2, Appli
45	540	55.9	1163	14	US-10-116-275-204	Sequence 204, App

ALIGNMENTS

RESULT 1

US-09-805-354-1
; Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH-AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1

Query Match 100.0%; Score 966; DB 10; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CPQEDSDIAFLIDSGSIIPHDPRMKGFSVTVMQOLKKSKTLFSLMQVSEBFRHFTPK 60
Db	1	CPQEDSDIAFLIDSGSIIPHDPRMKGFSVTVMQOLKKSKTLFSLMQVSEBFRHFTPK 60
Qy	61	BFQNNPNRSLVKPITQLLGRTHTTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db	61	BFQNNPNRSLVKPITQLLGRTHTTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120


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; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: NO. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match      100.0%; Score 966; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLFSIMQYSESFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLFSIMQYSESFRIHFTPK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 7
US-09-891-943-3
; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: NO. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-943-3

Query Match      100.0%; Score 966; DB 10; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLFSIMQYSESFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLFSIMQYSESFRIHFTPK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 8
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
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DB	264	DPLGYEDVIEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT	323
QY	181	IQNOLREKX 189	
DB	324	IQNOLREKI 332	
RESULT 10			
US-09-902-481A-6			
; Sequence 6, Application US/09902481A			
; Publication No. US2003005440A1			
; GENERAL INFORMATION:			
; APPLICANT: Springer, Timothy			
; APPLICANT: Shimaoka, Motomu			
; APPLICANT: Shifman, Julia			
; APPLICANT: Mayo, Stephen			
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY			
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK			
; CURRENT APPLICATION NUMBER: US/09/902,481A			
; CURRENT FILING DATE: 2001-07-09			
; PRIOR APPLICATION NUMBER: US 60/216,600			
; PRIOR FILING DATE: 2000-07-07			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 6			
; LENGTH: 1137			
; TYPE: PRT			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: synthetic			
US-09-902-481A-6			
Query Match 99.1%; Score 957; DB 10; Length 1137;			
Best Local Similarity 97.4%; Pred. No. 1.7e-91;			
Matches 184; Conservative 4; Mismatches 1; Indels 0; Gaps 0			
QY	1	CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKKTLFSLMOYSEEFRIHFTFK 60	
DB	128	CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKKTLFSLMOYSEEFRIHFTFK 187	
QY	61	EFQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFNITGARKNAFKILVITDGEKFG 120	
DB	188	EFQNNPNRSLVKPIITQLLGRTHATGVRKVIRELLNITNGARKNAFKILVITDGEKFG 247	
QY	121	DPLGYEDVIEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 180	
DB	248	DPLGYEDVIEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 307	
QY	181	IQNOLREKX 189	
DB	308	IQNOLREKI 316	
RESULT 11			
US-09-902-481A-5			
; Sequence 5, Application US/09902481A			
; Publication No. US2003005440A1			
; GENERAL INFORMATION:			
; APPLICANT: Springer, Timothy			
; APPLICANT: Shimaoka, Motomu			
; APPLICANT: Shifman, Julia			
; APPLICANT: Mayo, Stephen			
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY			
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK			
; CURRENT APPLICATION NUMBER: US/09/902,481A			
; CURRENT FILING DATE: 2001-07-09			
; PRIOR APPLICATION NUMBER: US 60/216,600			
; PRIOR FILING DATE: 2000-07-07			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 5			
; LENGTH: 1137			

TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-902-481A-5

Query Match 98.4%; Score 951; DB 10; Length 1137;
Best Local Similarity 95.2%; Pred. No. 7.1e-91;
Matches 180; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 60
DB 128 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 187

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247

QY 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307

QY 181 IQNQLREKX 189
DB 308 IQNQLREKI 316

RESULT 12
US-09-902-481A-4
Sequence 4, Application US/09902481A
Publication No. US2003005440A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.1
SEQ ID NO 4
LENGTH: 1137
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match 97.4%; Score 941; DB 10; Length 1137;
Best Local Similarity 94.7%; Pred. No. 8.1e-90;
Matches 179; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 60
DB 128 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 187

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247

QY 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307

QY 181 IQNQLREKX 189
DB 308 IQNQLREKI 316

RESULT 13
US-10-346-863-37
Sequence 37, Application US/10346863
Publication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0025447.4
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 37
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
US-10-346-863-37

Query Match 97.3%; Score 940; DB 15; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.5e-91;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMYSSEFRHFTFK 60

QY 65 NPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

QY 125 YEDVIPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 184
DB 121 YEDVIPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 185 LREKX 189
DB 181 LREKI 185

RESULT 14
US-10-615-515-9
Sequence 9, Application US/10615515
Publication No. US20040132974A1
GENERAL INFORMATION:
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2004
CURRENT APPLICATION NUMBER: US/10/615,515
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: PCT/GB02/00107
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: GB 0100750.9
PRIOR FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent in Ver. 3.2
SEQ ID NO 9
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
US-10-615-515-9

Query Match 97.3%; Score 940; DB 16; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.5e-91;

Matches	184;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	5	DSDI AFLIDGSGIIIPHDPRMKEFVSTVMEOQLKSKTFLFSMLQYSEEPRIHFTFKEFQN	64						
Dd	1	DSDI AFLIDGSGIIIPHDPRMKEFVSTVMEOQLKSKTFLFSMLQYSEEPRIHFTFKEFQN	60						
QY	65	NNPRSILVKPIITOLLGRTHYTATGIRKVVRLEFNITNGARKNAKILVIITDGEKFGDPGLG	124						
Dd	61	NNPRSILVKPIITOLLGRTHYTATGIRKVVRLEFNITNGARKNAKILVIITDGEKFGDPGLG	120						
QY	125	YEDVIPEADREGVIRYVIGVDAPFRSEKSQEELNTTIASKPPRHVFQOVNNFEALKTIONQ	184						
Dd	121	YEDVIPEADREGVIRYVIGVDAPFRSEKSQEELNTTIASKPPRHVFQOVNNFEALKTIONQ	180						
QY	185	LREXX 189							
Dd	181	LREKI 185							

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RESULT 15
US/10-346-863-17
; Sequence 17, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-17

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Query Match	97.2%;	Score 939;	DB 15;	Length 184;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-90;			
Matches 184; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	5	DSDIATFLDGS	SGSIIIPHD	FRMKEFEVSTWMEQLKSKTLEFSLMQYSEEPRIHTEKFQN 64	
Db	1	DSDIATFLDGS	SGSIIIPHD	FRMKEFEVSTWMEQLKSKTLEFSLMQYSEEPRIHTEKFQN 60	
QY	65	NNPRSLVKPI	TOLLGRTH	TATGIRKVVRLEFNI	TNGARKNAFKILVITDGEKFGDPLG 124
Db	61	NNPRSLVKPI	TOLLGRTH	TATGIRKVVRLEFNI	TNGARKNAFKILVITDGEKFGDPLG 120
QY	125	YEDVIPEADREGVIR	VIVGVGDFAFRSEKSQE	LNTASKPPRDHVQVNNF	EALKTIONQ 184
Db	121	YEDVIPEADREGVIR	VIVGVGDFAFRSEKSQE	LNTASKPPRDHVQVNNF	EALKTIONQ 180
QY	185	LREK	188		
Db	181	LREK	184		

Search completed: January 13, 2005, 15:39:44
Job time : 32.2304 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 9.08295 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWHULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLIDGSGSIIP.....FQVNFALKTIQNQLREXX 189

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	1152	2	US-08-476-062A-43
2	966	100.0	1152	5	PCT-US96-01314-43
3	966	100.0	1152	6	5424399-2
4	966	100.0	1153	1	US-08-173-497-3
5	966	100.0	1153	1	US-08-286-889-3
6	966	100.0	1153	1	US-08-485-618-3
7	966	100.0	1153	1	US-08-362-652-3
8	966	100.0	1153	2	US-08-605-672-3
9	966	100.0	1153	2	US-08-482-293A-3
10	966	100.0	1153	2	US-08-943-363-3
11	966	100.0	1153	3	US-09-193-043-3
12	966	100.0	1153	4	US-09-688-307A-3
13	966	100.0	1153	4	US-09-350-259-3
14	960	99.4	187	2	US-08-177-109A-61
15	960	99.4	187	2	US-08-687-706-61
16	934	96.7	216	4	US-09-795-872-5
17	934	96.7	435	5	PCT-US95-04439-1
18	595	61.6	1151	1	US-08-286-889-37
19	595	61.6	1151	1	US-08-485-618-37
20	595	61.6	1151	1	US-08-362-652-37
21	595	61.6	1151	2	US-08-605-672-37
22	595	61.6	1151	2	US-08-482-293A-37
23	595	61.6	1151	2	US-08-943-363-37
24	595	61.6	1151	3	US-09-193-043-37
25	595	61.6	1151	4	US-09-688-307A-37
26	595	61.6	1151	4	US-09-350-259-37
27	595	61.6	1161	1	US-08-485-618-55

28	595	61.6	1161	1	US-08-362-652-55	Sequence 55, Appl
29	595	61.6	1161	2	US-08-605-672-55	Sequence 55, Appl
30	595	61.6	1161	2	US-08-482-293A-55	Sequence 55, Appl
31	595	61.6	1161	2	US-08-943-363-55	Sequence 55, Appl
32	595	61.6	1161	3	US-09-193-043-55	Sequence 55, Appl
33	595	61.6	1161	4	US-09-688-307A-55	Sequence 55, Appl
34	595	61.6	1161	4	US-09-350-259-55	Sequence 55, Appl
35	594	61.5	413	1	US-08-485-618-101	Sequence 101, App
36	594	61.5	413	2	US-08-605-672-101	Sequence 101, App
37	594	61.5	413	2	US-08-482-293A-101	Sequence 101, App
38	594	61.5	413	2	US-08-943-363-101	Sequence 101, App
39	594	61.5	413	3	US-09-193-043-101	Sequence 101, App
40	594	61.5	413	4	US-09-688-307A-101	Sequence 101, App
41	594	61.5	413	4	US-09-350-259-101	Sequence 101, App
42	586	60.7	1155	1	US-08-286-889-46	Sequence 46, Appl
43	586	60.7	1155	1	US-08-485-618-46	Sequence 46, Appl
44	586	60.7	1155	1	US-08-362-652-46	Sequence 46, Appl
45	586	60.7	1155	2	US-08-605-672-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-08-476-062A-43
; Sequence 43, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Attract, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-476-062A-43

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Query Match      100.0%; Score 966; DB 2; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 1152
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US96-01314-43

Query Match      100.0%; Score 966; DB 5; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
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DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 3
5424399-2
; Patent No. 5424399
; APPLICANT: ARNAOUT, M. AMIN
; TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/78,871
; FILING DATE: 16-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 212,573
; FILING DATE: 28-JUN-1988
; SEQ ID NO: 2:
; LENGTH: 1152
5424399-2

Query Match      100.0%; Score 966; DB 6; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 4
US-08-173-497-3
; Sequence 3, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-173-497-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 5
US-08-286-889-3
; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 6
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFHFTFK 60
DB 144 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 7

US-08-362-652-3
Sequence 3, Application US/083622652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFHFTFK 60
DB 144 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 8

US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match 100.0%; Score 966; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 9

US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3

Query Match 100.0%; Score 966; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 10

US-08-943-363-3
Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 2; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IQNQLREKI 332

RESULT 11
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; PRIOR FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 3; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IQNQLREKI 332

RESULT 12
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3

Query Match
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IQNQLREKI 332

RESULT 13
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 4; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
Db 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLRE 187
Db 181 IQNQLRE 187

RESULT 15
US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-687-706-61

Query Match
Best Local Similarity 99.4%; Score 960; DB 2; Length 187;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
Db 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLRE 187
Db 181 IQNQLRE 187

RESULT 14
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-61

Query Match
Best Local Similarity 99.4%; Score 960; DB 2; Length 187;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
Db 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSESEFRHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLRE 187
Db 181 IQNQLRE 187
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Db	61	EFQNNENPRSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVWITDGEKFG	120
Qy	121	DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
Db	121	DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
Qy	181	IQNQLRE	187
Db	181	IQNQLRE	187

Search completed: January 13, 2005, 15:34:34
Job time : 10.0829 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 5.12706 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWHLB-C_COPY_144_320
Perfect score: 922
Sequence: 1 CPQEDSDIAFLIDGSGSIIP.....NTIASKPRDRHVQCNNFEC.177
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903	97.9	1153	1 RWHLB	cell surface glyco
2	692	75.1	1153	2 S00551	leukocyte surface
3	486	52.7	1163	1 RWHLB	cell surface glyco
4	309	33.5	1179	2 A52213	integrin alpha-E c
5	265.5	28.8	1170	2 S03308	cell surface glyco
6	245	26.6	1163	2 I56126	lymphocyte fuction
7	227	24.6	493	2 A33809	cartilage matrix p
8	222	24.1	500	2 S66522	cartilage matrix p
9	215	23.3	496	2 A37979	cartilage matrix p
10	196.5	21.3	3051	2 S42373	hypothetical prote
11	194.5	21.1	1747	2 A45974	collagen alpha 1(X
12	194.5	21.1	1857	2 S31212	collagen alpha 1(X
13	194.5	21.1	1888	2 S78476	collagen alpha 1(X
14	192	20.8	3124	2 A40020	collagen alpha 1(X
15	186.5	20.2	1151	2 A45226	integrin alpha-1 c
16	179.5	19.5	741	2 A45488	hypothetical prote
17	176.5	19.1	272	2 A55348	integrin alpha-1 -
18	171.5	18.6	1180	2 A35854	integrin alpha-1 c
19	164	17.8	929	2 I51027	type XII collagen
20	157.5	17.1	2944	2 A54849	collagen alpha 1(V
21	151	16.4	1170	2 I45914	integrin alpha 2 s
22	150.5	16.3	3137	2 A37797	collagen alpha 3(V
23	144	15.6	1181	2 A33998	integrin alpha-2 c
24	144	15.6	3176	2 CGHU3A	collagen alpha 3(V
25	141	15.3	1178	2 S44142	VLA-2 protein homo
26	138	15.0	550	2 T23760	hypothetical prote
27	136	14.8	371	2 S32604	collagen alpha 2(V
28	134.5	14.6	712	2 A45638	immunodominant mic
29	132	14.3	2813	1 VMHU	von Willebrand fac

ALIGNMENTS

RESULT 1

RWHLB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b)

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <COR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:G187284; PIDN:AAA59544.1; PID:G307148
A>Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1
A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:G186935; PIDN:AAA594;
A>Note: The authors translated the codon TAC for residue 1129 as Thr

R:Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regulated

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:G180018; PIDN:AAA58410.1; PID:G553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesion

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:89098893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:G189068; PIDN:AAA59903.1; PID:G386975

A>Note: part of this sequence was confirmed by protein sequencing
R:Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A:Reference number: A46526; MUID:93123748; PMID:8419480
A:Accession: A46526
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499,501-1153 <FLE>
A:Cross-references: GB:S52227; NID:9263047; PIDN:AA24821.1; PID:9263049
A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
A>Note: sequence extracted from NCBI backbone (NCBIP:121963)
R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
A:Reference number: A90664; MUID:87076671; PMID:3539202
A:Accession: A26091
A:Molecule type: protein
A:Residues: 17-31 <PIE>
A:Experimental source: granulocytes
R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A>Title: Characterization of the myeloid-specific CD11b promoter.
A:Reference number: I52567; MUID:92144986; PMID:1346576
A:Accession: I52567
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M84477; NID:9180184; PIDN:AA51960.1; PID:9553219
C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C:Genetics:
A:Gene: GDB:ITGAM; CR3A
A:Cross-references: GDB:120599; OMIM:120980
A:Map position: 16p11.2-16p11.2
A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homodimer; mag
C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F:17-1108/Domain: extracellular #status predicted <EXT>
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:465-473/Region: calcium/magnesium binding #status predicted
F:530-538/Region: calcium/magnesium binding #status predicted
F:593-601/Region: calcium/magnesium binding #status predicted
F:1109-1134/Domain: transmembrane #status predicted <TMM>
F:1135-1153/Domain: intracellular #status predicted <INT>
F:86,240,391,469,693,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 5.6e-72;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 60
DB 144 CPQSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 203

QY 61 EFQNNPNSRLVKPTQLGRTHATGIRKVVRELFNTNGARKNAKILVITDGEKFG 120
DB 204 EFQNNPNSRLVKPTQLGRTHATGIRKVVRELFNTNGARKNAKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 319

RESULT 2
S00551
Leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
N:Alternate names: complement-3 receptor alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00551; I59078

R:Pytela, R.
EMBO J. 7, 1371-1378, 1988
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
A:Reference number: S00551; MUID:88312584; PMID:3044779
A:Accession: S00551
A:Molecule type: DNA
A:Residues: 1-1153 <PYT>
A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A>Note: the authors translated the codon CAC for residue 569 as Gln
R:Satre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
A:Reference number: I59078; MUID:86287312; PMID:2942940
A:Accession: I59078
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11-44 <RES>
A:Cross-references: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
C:Genetics:
A:Gene: Mac-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homod
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1106-1129/Domain: transmembrane #status predicted <TMM>

Query Match 75.1%; Score 692; DB 2; Length 1153;
Best Local Similarity 77.3%; Pred. No. 3e-53;
Matches 136; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 1 CPQSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 60
DB 144 CPQSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 203

QY 61 EFQNNPNSRLVKPTQLGRTHATGIRKVVRELFNTNGARKNAKILVITDGEKFG 120
DB 204 DFKNPSPRSHVSPIKOLNGRTKTASGIRKVVRELFHTKNGARENAKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 319

RESULT 3
RWHULC
cell surface glycoprotein CD11c precursor - human
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A36584; A35543; S00864
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A36584
A:Contents: erratum
A:Accession: A36584
A:Molecule type: DNA
A:Residues: 1-1163 <COR>
A:Cross-references: UNIPROT:P20702
A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A:Reference number: A35543; MUID:90153906; PMID:2303426
A:Accession: A35543
A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A>Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A>Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166645; PMID:3327687
A:Accession: S00864

A:Molecule type: mRNA
A:Residues: 1-755, 'L', 757-1163 <CO3>
A:CROSS-references: GB:M81695; EMBL:Y00093; NID:G487829; PIDN:AAA59180.1; PID:G487830
A>Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:CROSS-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homolog
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:1108-1133/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 52.7%; Score 486; DB 1; Length 1163;
Best Local Similarity 53.4%; Pred. No. 6e-35;
Matches 94; Conservative 33; Mismatches 49; Indels 0; Gaps 0;
QY 1 CPQEDSIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEBFRIHFTPK 60
DB 145 CPQEQDIVFLIDSGSISRRNFATMNFVRAVISQFORPSTQFSLMOFSNKKFQTHFTFE 204
QY 61 EFQNNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 205 EFRRTSNPLSLASHVQLQGFYTTATQNVVHFLFASGARRATKILVITDGEKFG 264
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 176
DB 265 DSLDYKDVIPMAAGIIRYAIYGLVGLAFONRNSWELNDIASKPSQEHFKVEDFD 320
RESULT 4
A53213
Integrin alpha-E chain - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
R:Shaw, S.K.; Cepke, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A:Reference number: A53213; MUID:94164962; PMID:8119947
A:Accession: A53213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:CROSS-references: UNIPROT:P38570; GB:L25851; NID:G457244; PID:G457245
C:Genetics:
A:Gene: GDB:ITGAE
A:CROSS-references: GDB:330801
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homolog
F:199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
Query Match 33.5%; Score 309; DB 2; Length 1179;
Best Local Similarity 38.4%; Pred. No. 3.2e-19;
Matches 66; Conservative 39; Mismatches 65; Indels 2; Gaps 1;
QY 6 SDIAFLIDSGSIIPHDPRMKEFVSTVMEQL--KKSKTLFSLMOYSEBFRIHFTKBFQ 63
DB 201 TEAIIIDSGSIDPDPORAKDFISNMWNYEKCFCFNALVQGVIGVITQFEDLRDQ 260
QY 64 NNPNSRLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
DB 261 DVWASLARQNTQVGSVTKTASAMQHVLDSIFTSHGSRKASKVMVVLTDGGIFEDPL 320
QY 124 GYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPF 175
DB 321 NLTTVINSRPMQGVVERFAIGVGBEFPKARTARELNLIASDPDETHAFKVTNY 372

RESULT 5

S03308
cell surface glycoprotein CD11a precursor - human
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:CROSS-references: UNIPROT:P20701; UNIPROT:09UBC8; EMBL:Y00796; NID:G31421; PIDN:CAA6874
A>Note: part of this sequence was confirmed by protein sequencing
R:Corneil, R.D.; Gollan, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pr
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:130863)
R:Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A:Title: Identification of cell-specific and developmentally regulated nuclear factors t
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:CROSS-references: GB:M95609
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 19305-19311, 1993
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NUE>
A:CROSS-references: EMBL:Z22804; NID:G311405; PIDN:CAA80461.1; PID:G311406
C:Genetics:
A:Gene: GDB:ITGAL; CD11A
A:CROSS-references: GDB:119757; OMIM:153370
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homolog
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <
F:154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 28.8%; Score 265.5; DB 2; Length 1170;
Best Local Similarity 33.0%; Pred. No. 2.3e-15;
Matches 58; Conservative 44; Mismatches 67; Indels 7; Gaps 2;
QY 1 CPQEDSIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEBFRIHFTPK 60
DB 150 CIKGNVLDVFLFDGSMVLPDEFQKILDFMKDMKLSNTSYQFAAVQFSTYKTEFDFS 209
QY 61 EFQNNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 210 DYVKWKPDPALLKHVKHMLLTNTFGAINYVATEVREELGARPDPATKLLIITDGE--A 267
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 176
DB 268 TDSGNDAKD-----IIRYIIGIKHFKQTESQETLHKFASKPASEFVKILDTFE 318
RESULT 6
I56126
lymphocyte fuction-associated molecule-1-alpha - mouse
C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I56126
R/Kaufmann, Y.; Teeng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A/Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit A
A/Reference number: I56126; MUID:91268576; PMID:2051027
A/Accession: I56126
A/Status: preliminary; translated from GB/EMBL/DBBJ
A/Molecule type: mRNA
A/Residues: 1-1163 <RES>
A/Cross-references: UNIPROT:P24063; GB:M60778; NID:gl98785; PIDN:AAA39426.1; PID:gl98786

C/Genetics:
A/Gene: LFA-1
C/Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homology
F/151-315/Domain: von Willebrand factor type A repeat homology <VMA1>

Query Match 26.6%; Score 245; DB 2; Length 1163;
Best Local Similarity 32.6%; Pred. No. 1.5e-13;
Matches 60; Conservative 35; Mismatches 67; Indels 22; Gaps 3;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFTFK 60

DB 147 CMKGKVDLVFLFDGSGSLDRKDFEKLPEMKDVMKLSNTSYQPAVQFSTDCRTEFTFL 206

QY 61 EF-QNNPNSRLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEK 119

DB 207 DYVKQKNPDVLLGVSQPMFLTLNTFRAINVVAHVFEESGARDATKVLVITDGD--- 263

QY 120 GDPLGYEDVIPADREG-----VIRYVIGVDGAFRSEKSRQELNTTASKPRDHVQC 172

DB 264 -----BASDKGNISAAHDITRYIIGKHGKHFVSQKQKTLHFASPEVSEFVKIL 312

QY 173 NNFE 176

DB 313 DTFE 316

RESULT 7

A33809

cartilage matrix protein precursor - chicken

C/Species: Gallus gallus (chicken)

C/Date: 09-Mar-1990.#sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C/Accession: A33809; A26364

R/Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argu

J. Biol. Chem. 264, 8126-8134, 1989

A/Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex

grins. Von Willebrand factor, complement factors B and C2, and epidermal growth factor.

A/Reference number: A33809; MUID:89255246; PMID:2542265

A/Accession: A33809

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-493 <KIS>

A/Cross-references: UNIPROT:P05099; GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235

R/Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987

A/Title: Structural features of cartilage matrix protein deduced from cDNA.

A/Reference number: A26364; MUID:87092429; PMID:3025875

A/Accession: A26364

A/Molecule type: mRNA

A/Residues: 78-493 <ARG>

A/Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546

C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe

F/37-204/Domain: von Willebrand factor type A repeat homology <VMA1>

F/225-260/Domain: EGF homology <EGF>

F/270-434/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 24.6%; Score 227; DB 2; Length 493;

Best Local Similarity 32.0%; Pred. No. 2.1e-12;

Matches 56; Conservative 35; Mismatches 66; Indels 18; Gaps 4;

QY 7 DIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKS--KTLFSLMOYSEFRHFTFKFQN 64

DB 272 DLVFLIDGSKSVRPENFELVKKFINQIVSEVSEKQAQGLVQYSSVRQEPFLGQFKN 331

QY 65 NPNPSRLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124

DB 332 KDOIKAAYKKWAYMEKGTMTQALKYLVDSSFSIANGARPGVPKGVITFDGRS----- 385

QY 125 YEDVIPADRE---GVIRYVIGVDGAFRSEKSRQELNTTASKPRDRHVQCNNF 175

DB 386 -QDYITDAAKKAKDLGPRMFAVGGNV-----EDELREIASEPVAEHVFTADF 434

RESULT 8

S66522

cartilage matrix protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S66522

R/Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.

Eur. J. Biochem. 236, 970-977, 1996

A/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c

A/Reference number: S66522; MUID:96270751; PMID:8665920

A/Accession: S66522

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-500 <ASZ>

A/Cross-references: UNIPROT:P51942; EMBL:U35035; NID:gl163178; PIDN:AA06521.1; PID:gl163

C/Genetics:

A/Gene: CMP

C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-500/Product: cartilage matrix protein #status predicted <MAT>

F/43-210/Domain: von Willebrand factor type A repeat homology <VMA1>

F/231-266/Domain: EGF homology <EGF>

F/277-441/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 24.1%; Score 222; DB 2; Length 500;

Best Local Similarity 30.5%; Pred. No. 5.9e-12;

Matches 54; Conservative 39; Mismatches 66; Indels 18; Gaps 4;

QY 6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTL--FSLMOYSEFRHFTFKFQ 63

DB 278 TDLVFLIDGSKSVRPENFELVKKFINQIVLVDLSDRLAQVLQVYSSIRQEPFLGRFH 337

QY 64 NPNPSRLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123

DB 338 SKDOIKAARVNNYMEKGTMTGAALKYLLIDNFTVSSGARPGCAQKGVITFDGRS----- 392

QY 124 GYEDVIPADRE---GVIRYVIGVDGAFRSEKSRQELNTTASKPRDRHVQCNNFE 176

DB 393 --QDYINDAARKAKDLGPRMFAVGGNV-----EDELREIASEPVAHDYFTADF 442

RESULT 9

A37979

cartilage matrix protein precursor - human

C/Species: Homo sapiens (man)

C/Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004

C/Accession: A37979; B37979

R/Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shc

J. Biol. Chem. 265, 19624-19631, 1990

A/Title: Structure and chromosomal location of the human gene encoding cartilage matrix I

A/Reference number: A37979; MUID:91060568; PMID:2246248

A/Accession: A37979

A/Molecule type: DNA

A/Residues: 1-496 <JEN>

A/Cross-references: UNIPROT:P21941; GB:J05667

A/Accession: B37979

A/Molecule type: mRNA

A/Residues: 157-290, 'L', 292-496 <JEN2>

A/Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:gl80651; PIDN:AAA63904.1; PID:gl

C/Genetics:

A/Gene: GDB:CRM

A/Cross-references: GDB:127280; OMIM:115437

A/Map position: lp35-1p35

A:Introns: 32/1; 147/3; 222/3; 264/1; 403/1; 454/1; 481/1
C:Complex: homotrimer
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
C:Keywords: glycoprotein; homotrimer
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-496/Product: cartilage matrix protein #status predicted <MAT>
F:39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F:227-262/Domain: EGF homology <EGF>
F:273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F:76,344/Binding site: carbohydrate (Aan) (covalent) #status predicted
F:221-236,234-247,249-262/Disulfide bonds: #status predicted

Query Match 23.3%; Score 215; DB 2; Length 496;
Best Local Similarity 29.9%; Pred. No. 2.5e-11;
Matches 53; Conservative 38; Mismatches 68; Indels 18; Gaps 4;

QY 6 SDIAFLDGGSGIIIPHDPRRMKEFVSTVMEQLKKSKTL--PSLMQYSEFRTHETFKRFQ 63
DB 274 TDLVFLDGGSKVRPENFELVKKFIQIVDTLDVSDKLAQVGLVQYSSVROEFPFLGRFH 333
QY 64 NNPNRSLVKPTITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
DB 334 TKDKIAAVRNNSYMEKGTMTGAALKYLIDNSTVTSRGARPGAKVGIVFTDGRS---- 388

QY 124 GYEDVIPADRE-----GVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQCNFPE 176
DB 389 --QDYINDAAKAKDLGFMFAGVGNV-----EDELREIASEPVAEHFYFTADFK 438

RESULT 10
S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C:Accession: S42373
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-1051 <SMI>
A:Cross-references: EMBL:Z30423; NID:G458479; PID:G458485
C:Genetics:
A:Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
F:512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F:754-793/Domain: fibronectin type II repeat homology <2F1>
F:1201-1244/Domain: EGF homology <EGF>

Query Match 21.3%; Score 196.5; DB 2; Length 3051;
Best Local Similarity 32.2%; Pred. No. 1e-08;
Matches 57; Conservative 36; Mismatches 61; Indels 23; Gaps 7;

QY 1 CPQEDSDIAFLDGGSGIIPHDPRRMKEFVSTVMEQLKKSKTLPSLMQYSEFRTH 55
DB 508 CPQKTDLVFLDGGSGIYGVKNEVRFVFE--LFEIGRSKTRVGLIQYSDQIRH 565
QY 56 HPTFEFQNNPNRSLVKPITO---LLGRTHATGIRKVVRELFNITNGAR---KNAPKI 109
DB 566 EFDLDQYGDGD---SLLKGISITQVLTGLTRGAAIQHVQSGFERRGARQQQSDIARV 622

QY 110 LVVITDGEKFGDPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPR 166
DB 623 AIIITDGRSQDNVTGPAD---SARKLSINTFAIGVTDHVLVLA---SELESIAGSPNR 672

RESULT 11
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N:Alternate names: undulin
C:Species: Gallus gallus (Chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A45974; S30085; S22916; S17035; S20833
R:Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin

J. Biol. Chem. 268, 12177-12184, 1993
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' regions
A:Reference number: A45974; MUID:93280195; PMID:8505337
A:Accession: A45974
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-1747 <GER>
A:Cross-references: UNIPROT:P32018
A:Experimental source: embryo skin
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBI:133365)
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30085
A:Molecule type: mRNA
A:Residues: 1472-1660 <APT>
A:Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G938175
R:Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A:Title: Type XIV collagen is a variant of undulin.
A:Reference number: S22916; MUID:92339443; PMID:1339349
A:Accession: S22916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F.
Eur. J. Biochem. 201, 333-338, 1991
A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A:Reference number: S17035; MUID:92037585; PMID:1935930
A:Accession: S17035
A:Molecule type: mRNA
A:Residues: 1472-1659 <GOR1>
A:Accession: S20833
A:Molecule type: protein
A:Residues: 1551-1570; 1593-1599; 1639-1667 <GOR2>
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:236-317/Domain: fibronectin type III repeat homology <FN3A>
F:326-409/Domain: fibronectin type III repeat homology <FN3B>
F:418-498/Domain: fibronectin type III repeat homology <FN3C>
F:507-591/Domain: fibronectin type III repeat homology <FN3D>
F:625-707/Domain: fibronectin type III repeat homology <FN3E>
F:716-798/Domain: fibronectin type III repeat homology <FN3F>
F:806-893/Domain: fibronectin type III repeat homology <FN3G>
F:924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 21.1%; Score 194.5; DB 2; Length 1747;
Best Local Similarity 31.8%; Pred. No. 7.6e-09;
Matches 57; Conservative 28; Mismatches 83; Indels 11; Gaps 4;

QY 1 CPQEDSDIAFLDGGSGIIPHDPRRMKEFVSTVMEQLKKSKTLPSLMQYSEFRTH 57
DB 920 CKAARADLVFLVDGSGIDNFKIISFLYTGALDKIGDPGTQVAILQFSDDPRTEF 979
QY 58 TFKEFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGE 117
DB 980 KLNAYKTETLEAIQQIAYKGGNTKTGAIKHAREVLFTGBAGMRKGPVKLVWITDGR 1039
QY 118 KFGDPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQCNFPE 176
DB 1040 SQDD---VNKVSREMLQDGFSEFALGVADADYS-----ELVNIGKPSERHVFVDDDFD 1090

RESULT 12
S31212
collagen alpha 1(XIV) chain precursor, short form - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003

C;Accession: S31212
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31212
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-1857 <WAE>
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
A;Gene: Coll14A1
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <WAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWAL>
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWAL2>
C;Accession: S31211
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416,1460-1811,1843-1888 <WAE>
A;Cross-references: EMBL:X70793
C;Genetics:
A;Gene: Coll14A1
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <WAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWAL>

F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWAL2>
Query Match 21.1%; Score 194.5; DB 2; Length 1888;
Best Local Similarity 31.8%; Pred. No. 8.4e-09;
Matches 57; Conservative 28; Mismatches 83; Indels 11; Gaps 4;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKRFV-STV--MEOLKSKTLFSLMOYSEFRIFHF 57
Db 1036 CAAKADLVFLVDGWSIGDGNFNKLIISFLYSTVGALDKIGDPGTQVAIIQSDDPRTF 1095
QY 58 TPKFQNNPNRSLVKTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVITDGE 117
Db 1096 KLNAYKTETLEAQIAYKGGNTKTGKAHKAREVLFTGEAGMRKGIPKVLVITDGR 1155
QY 118 KFGDPLGYEDVPEADREGVIRYVVGDAFSEKSRQELNTIASKPRDRHVQCNNFE 176
Db 1156 SQDD---VNKVSREMQLDGFSFAIGVADADYS-----ELVNIIGSKPSERHVFVDDFD 1206
RESULT 14
A40020
collagen alpha 1(XII) chain precursor - chicken
N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obara
J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
A;Molecule type: mRNA
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BA00701.1; PID:g222811
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
A;Molecule type: mRNA
A;Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c
A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037
A;Molecule type: mRNA
A;Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A;Note: this sequence has been revised in reference A34485
R;Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of t
A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
A;Molecule type: protein
A;Residues: 'X', 1333, 'Q', 1335-1347;1914-1928;2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <
R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peptin-

Search completed: January 13, 2005, 15:13:31
Job time : 6.12706 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 37.0546 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-C_COPY_144_320
Perfect score: 922
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....NTIASKPRDRHVQCNPFC.177

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	903	97.9	1152	1	ITAM_HUMAN	P11215 homo sapien
2	722	78.3	920	2	Q28984	Q28984 sus scrofa
3	692	75.1	1153	1	ITAM_MOUSE	P05555 mus musculus
4	669	72.6	1151	2	Q9J130	Q9J130 rattus norv
5	550	59.7	1161	1	ITAD_RAT	Q9QY67 rattus norv
6	545	59.1	1162	1	ITAD_HUMAN	P13349 homo sapien
7	533	57.8	205	2	Q63001	Q63001 rattus norv
8	486	52.7	1163	1	ITAX_HUMAN	P20702 homo sapien
9	483	52.4	1188	2	Q6KAS4	Q6KAS4 mus musculus
10	483	52.4	1188	2	BAD21383	Bad21383 mus muscu
11	482	52.3	1169	1	ITAX_MOUSE	Q9QX44 mus musculus
12	408	44.3	304	2	Q6PG66	Q6PG66 mus musculus
13	408	44.3	304	2	AAH57200	Aah57200 mus muscu
14	322	34.9	895	2	Q9WUF8	Q9WUF8 mus sp. itg
15	322	34.9	1038	2	Q8BS01	Q8BS01 mus musculus
16	322	34.9	1167	2	Q88340	Q88340 rattus norv
17	319	34.6	231	2	Q8N882	Q8N882 homo sapien
18	316	34.3	1167	1	ITAE_MOUSE	Q60677 mus musculus
19	309	33.5	1179	1	ITAE_HUMAN	P38570 homo sapien
20	307	33.3	1160	2	Q8MKF4	Q8MKF4 felis silve
21	301.5	32.7	1167	2	Q88341	Q88341 rattus norv
22	269.5	29.2	1170	1	ITAL_HUMAN	P20701 homo sapien
23	262.5	28.5	1165	1	ITAL_BOVIN	P61625 bos taurus
24	256	27.8	269	2	Q80WE9	Q80WE9 rattus norv
25	245	26.6	1160	2	Q9R200	Q9R200 mus musculus
26	245	26.6	1161	2	Q9WTV4	Q9WTV4 mus musculus
27	245	26.6	1163	1	ITAL_MOUSE	P24063 mus musculus
28	240.5	26.1	1196	2	Q9RTF1	Q9RTF1 cyprinus ca
29	238.5	25.9	1166	2	Q6TYB8	Q6TYB8 bos taurus
30	238.5	25.9	1166	2	AAQ90015	Aaq90015 bos tauru
31	238	25.8	257	2	Q8C270	Q8C270 mus musculus

32	235	25.5	79	2	Q8HY27	Q8hy27 ovis aries
33	235	25.5	79	2	Q8HY41	Q8hy41 bos taurus
34	227	24.6	493	1	CAMA_CHICK	P05099 gallus gall
35	226.5	24.6	1187	2	Q98TF0	Q98tf0 cyprinus ca
36	222.5	24.1	652	2	Q95LI2	Q95li2 bos taurus
37	222	24.1	500	1	CAMA_MOUSE	P51942 mus musculus
38	222	24.1	500	2	Q8OVN5	Q8OVN5 mus musculus
39	220.5	23.9	656	2	Q96DT1	Q96dt1 homo sapien
40	220.5	23.9	678	2	Q9UDN0	Q9udn0 homo sapien
41	220.5	23.9	678	2	AAQ88704	Aaq88704 homo sapi
42	220.5	23.9	693	2	Q96DM8	Q96dm8 homo sapien
43	215	23.3	496	1	CAMA_HUMAN	P21941 homo sapien
44	210.5	22.8	650	2	Q8VHI5	Q8vhi5 mus musculus
45	208.5	22.6	628	2	Q8BQ41	Q8bq41 mus musculus

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (leukocyte adhesion receptor MOI)
DE (Neutrophil adherence receptor).
GN Name=ITGAM; Synonyms=CR3A, CD11B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=8909893; PubMed=2563162;
RA Hackett D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
RN [6]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaut M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and
RT developmentally regulated expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
RN [7]
RP SEQUENCE OF 1-9 FROM N.A.
RX TISSUE=Blood;
RX MEDLINE=92144986; PubMed=1346576;
RA Pahl H.L., Rosmarin A.G., Tenen D.G.;
RT "Characterization of the myeloid-specific CD11b promoter.";
RL Blood 79:865-870(1992).
RN [8]
RP SEQUENCE OF 17-31.
RX MEDLINE=87076671; PubMed=3539202;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
RT across species and homology to platelet IIB/IIIA.";
RL Biochim. Biophys. Acta 874:368-371(1986).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RX MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Kieu P., Arnaut M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
RT CR3 (CD11b/CD18).";
RL Cell 80:631-638(1995).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RX MEDLINE=96363671; PubMed=8747450;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RT activation?";
RL Structure 3:1333-1340(1995).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RX MEDLINE=98362595; PubMed=9687375;
RA Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
RA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
RA Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
RA Mutchler V.T., Tonich C.S., Watenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
RT assessment.";
RL Structure 6:923-935(1998).
RN [12]
RP 3D-STRUCTURE MODELING OF 17-616.
RX MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunits and a calcium binding site on its lower surface.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).
CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
CC adhesive interactions of monocytes, macrophages and granulocytes
CC as well as in mediating the uptake of complement-coated particles.
CC It is identical with CR-3, the receptor for the iC3b fragment of
CC the third complement component. It probably recognizes the R-G-D
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
CC of fibrinogen gamma chain.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
CC associates with beta-2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11b.htm".

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CC -----
CC EMBL; J03925; AAA59544.1; -;
CC EMBL; M18044; AAA59491.1; -;
CC EMBL; J04145; AAA59903.1; -;
CC EMBL; S52277; AAB24821.1; -;
CC EMBL; S52152; AAB24821.1; JOINED.
CC EMBL; S52153; AAB24821.1; JOINED.
CC EMBL; S52154; AAB24821.1; JOINED.
CC EMBL; S52155; AAB24821.1; JOINED.
CC EMBL; S52157; AAB24821.1; JOINED.
CC EMBL; S52159; AAB24821.1; JOINED.
CC EMBL; S52161; AAB24821.1; JOINED.
CC EMBL; S52164; AAB24821.1; JOINED.
CC EMBL; S52165; AAB24821.1; JOINED.
CC EMBL; S52167; AAB24821.1; JOINED.
CC EMBL; S52169; AAB24821.1; JOINED.
CC EMBL; S52170; AAB24821.1; JOINED.
CC EMBL; S52173; AAB24821.1; JOINED.
CC EMBL; S52174; AAB24821.1; JOINED.
CC EMBL; S52180; AAB24821.1; JOINED.
CC EMBL; S52181; AAB24821.1; JOINED.
CC EMBL; S52184; AAB24821.1; JOINED.
CC EMBL; S52189; AAB24821.1; JOINED.
CC EMBL; S52191; AAB24821.1; JOINED.
CC EMBL; S52192; AAB24821.1; JOINED.
CC EMBL; S52203; AAB24821.1; JOINED.
CC EMBL; S52212; AAB24821.1; JOINED.
CC EMBL; S52213; AAB24821.1; JOINED.
CC EMBL; S52216; AAB24821.1; JOINED.
CC EMBL; S52219; AAB24821.1; JOINED.
CC EMBL; S52220; AAB24821.1; JOINED.
CC EMBL; S52221; AAB24821.1; JOINED.
CC EMBL; S52222; AAB24821.1; JOINED.
CC EMBL; S52226; AAB24821.1; JOINED.
CC EMBL; M76724; AAA58410.1; -;
CC EMBL; M84477; AAA51960.1; -;
CC PIR; A31108; RWHU1B.
CC PDB; 1A8X; Model; @=17-1152.
CC PDB; 1BHO; X-ray; 1/2=-.
CC PDB; 1BHQ; X-ray; 1/2=-.
CC PDB; 1IDN; X-ray; 1/2=-.
CC PDB; 1IDO; X-ray; @=140-331.
CC PDB; 1JLM; X-ray; @=143-334.
CC PDB; 1MIU; X-ray; A=137-331.
CC PDB; 1NF7; X-ray; A=144-337.
CC PDB; 1N9Z; X-ray; A=140-335.
CC PDB; 1NAS; X-ray; A=144-345.
CC Genew; HGNC:6149; ITGAM.
CC MIM; 120980; -;
CC GO; GO:0008305; C:integrin complex; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC InterPro; IPR000413; Integrin_alpha.
CC InterPro; IPR002035; VWFA.
CC Pfam; PF01839; FG-GAP; 3.
CC Pfam; PF00357; Integrin_alpha; 1.
CC Pfam; PF00092; VWFA; 1.
CC PRINTS; PR01185; INTEGRINA.
CC PRINTS; PR00453; VWFADOMAIN.
CC PRINTS; PR00191; Int_alpha; 5.
CC SMART; SM00327; VWFA; 1.
CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE; PS50234; VWFA; 1.
CC 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
CC Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
CC Transmembrane.

```
FT SIGNAL 1 16 Integrin alpha-M.
FT CHAIN 17 1152

Query Match
Best Local Similarity 97.9%; Score 903; DB 1; Length 1152;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPQSDIAFLIDGSGSIIPHDPRMKGFVSTVMSQLKSKTKTLFSLMYSSEFRTHFTFK 60
Db 144 CPQSDIAFLIDGSGSIIPHDPRMKGFVSTVMSQLKSKTKTLFSLMYSSEFRTHFTFK 203

Qy 61 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

Qy 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPDRHVFQCNFFE 176
Db 264 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPDRHVFQCNFFE 319

RESULT 2
Q28984 PRELIMINARY; PRT; 920 AA.
AC Q28984
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CD11b (Fragment).
GN Name=CD11b;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.-K., Schook L.B., Rutherford M.S.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; U40072; AAB16869.1; -
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR00413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWPA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 920
SQ SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;

Query Match
Best Local Similarity 80.1%; Score 722; DB 2; Length 920;
Matches 141; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CPQSDIAFLIDGSGSIIPHDPRMKGFVSTVMSQLKSKTKTLFSLMYSSEFRTHFTFK 60
Db 11 CPQSDIAFLIDGSGSIINRLDFQRMKGFVSTVMSQGFQKSKTKTLFALMQYSEDFYTHFTFN 70

Qy 61 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 71 DFKRPNPSKLLVRPRLQLLGRTHHTATGIRKVVRELFHSGSGARENALKILVITDGEKFG 130

Qy 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPDRHVFQCNFFE 176
Db 131 DPLGYEDVPEADREGVIRYVIGVGDAFNWSKRELNLTIASKPCGDHVFQCNFFE 186
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RESULT 3
ITAM_MOUSE
ID ITAM_MOUSE STANDARD; PRT; 1153 AA.
AC P05555; O8CAV73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
DE subunit (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name=Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88312584; PubMed=3044779;
RA Pytela R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
RL EMBO J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Naka K., Tomaru Y., Hasegawa Y., Suzuki H., Yamana H., Gojohori T., Baldarelli R., Hill D.P., Sult C., Hume D.A., Quackenbush J., Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda I., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 11-45 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=86287312; PubMed=2942940;
RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.;
RT "A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
RN [4]
RP SEQUENCE OF 17-28.
RX MEDLINE=85188276; PubMed=3887182;
RA Springer T.A., Teplow D.B., Dreyer W.J.;
RT "Sequence homology of the LPA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon.";
RL Nature 314:540-542(1985).
CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes
```


as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in mast cell development and in immune complex-mediated glomerulonephritis. Mice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophil accumulation, in response to an impaired degranulation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop obesity.

-!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M associates with beta-2.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

Isoid=P05555-1; Sequence=Displayed;

Name=2;

Isoid=P05555-2; Sequences=VSP_010473;

Notes=No experimental confirmation available;

-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and granulocytes.

-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

-!- SIMILARITY: Belongs to the integrin alpha chain family.

-!- SIMILARITY: Contains 7 FG-GAP repeats.

-!- SIMILARITY: Contains 1 VWFA domain.

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EMBL; X07640; CAA30479.1; -.

EMBL; AK039444; BAC30350.1; -.

EMBL; M14293; AAA39484.1; -.

PIR; S00551; S00551.

HSSP; P11215; 1BHQ.

MGI; 96607; Itgam.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0007155; P:cell adhesion; IMP.

GO; GO:0045123; P:cellular extravasation; IMP.

GO; GO:0030593; P:neutrophil chemotaxis; IMP.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR02035; VWF A.

Pfam; PF01839; FG-GAP; 3.

Pfam; PF00357; Integrin_alpha; 1.

Pfam; PF00092; VWA; 1.

PRINTS; PR01185; INTEGRINA.

PRINTS; PR00453; VWFADOMAIN.

SMART; SM00191; Int_alpha; 5.

SMART; SM00327; VWA; 1.

PROSITE; PS00242; INTEGRIN_ALPHA; 1.

PROSITE; PS0234; VWFA; 1.

Alternative splicing; Calcium; Cell adhesion;

Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;

Signal; Transmembrane.

SIGNAL 1 16

CHAIN 17 1153 Integrin alpha-M.

DOMAIN 17 1105 Extracellular (Potential).

TRANSMEM 1106 1129 Potential.

DOMAIN 1130 1153 Cytoplasmic (Potential).

REPEAT 31 84 FG-GAP 1.

REPEAT 85 163 FG-GAP 2.

DOMAIN 164 350 VWA.

REPEAT 337 400 FG-GAP 3.

REPEAT 401 452 FG-GAP 4.

REPEAT 454 515 FG-GAP 5.

REPEAT 517 575 FG-GAP 6.

REPEAT 580 632 FG-GAP 7.

FT CA_BIND 465 473 Potential.

FT CA_BIND 529 537 Potential.

FT CA_BIND 592 600 Potential.

FT SITE 1132 1136 GFFKR motif.

FT DISULFID 66 73 By similarity.

FT DISULFID 105 123 By similarity.

FT DISULFID 654 711 By similarity.

FT DISULFID 770 776 By similarity.

FT DISULFID 999 1023 By similarity.

FT DISULFID 1028 1033 By similarity.

FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 772 772 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 801 801 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 881 881 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 941 941 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 980 980 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 994 994 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1022 1022 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1051 1051 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1076 1076 N-linked (GlcNAc...) (Potential).

FT VARSPLIC 453 569 Missing (in isoform 2).

FT CONFLICT 37 37 N -> S (in Ref. 2).

FT CONFLICT 683 683 V -> G (in Ref. 2).

SQ SEQUENCE 1153 AA; 127480 MW; 178DB988AECB0343 CRC64;

Query Match 75.1%; Score 692; DB 1; Length 1153;

Best Local Similarity 77.3%; Pred. No. 3.6e-49;

Matches 136; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKKSKTLFSLMQYSEPRHFTFK 60

DB 144 CPQESDIVLIDGSGSINNIDFQKMEFVSTVMEQFKSKTLFSLMQYSDSEPRHFTFN 203

QY 61 BFQNNPRLSVKPIITQLLGHGTHATGIRKVVRLFNITGARKNAKILVITDGEKFG 120

DB 204 DFKRNPSPRSHVSPIKQLNGTKTASGIRKVVRLFNITGARKNAKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRVYGVGDAPRSEKSEQLNTIASKPPRHVFCNNFE 176

DB 264 DPLDYKDVIPADRAGVIRVYGVGNFAFNKPSRELDITASKPAGEHVFOVDNFE 319

RESULT 4

Q9J130 PRELIMINARY; PRT; 1151 AA.

AC Q9J130

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Integrin beta 2 alpha subunit.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Fathallah D.M. Sr., Zerria K. Jr.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBAJ databases.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

DR EMBL; AF268593; AAF81280.1; -.

DR HSSP; P11215; 1BHQ.

DR GO; GO:0008305; C:integrin complex; IEA.

DR GO; GO:0007160; P:cell-matrix adhesion; IEA.

DR	GO: GO:0007229; P-integrin-mediated signaling pathway; IEA.	CC	EMBL; AF021334; AAF21241.1; --
DR	InterPro; IPR000413; Integrin_alpha.	DR	HSSP; P11215; 1BHQ.
DR	InterPro; IPR000413; Integrin_alpha.	DR	InterPro; IPR000413; Integrin_alpha.
DR	Pfam; PF01839; FG-GAP; 2.	DR	Pfam; PF01839; FG-GAP; 3.
DR	Pfam; PF00092; VWA; 1.	DR	Pfam; PF00092; VWA; 1.
DR	PRINTS; PR01185; INTEGRINA.	DR	PRINTS; PR01185; INTEGRINA.
DR	PRINTS; PR00453; VWFADOMAIN.	DR	PRINTS; PR00453; VWFADOMAIN.
DR	SMART; SM00191; Int_alpha; 1.	DR	SMART; SM00191; Int_alpha; 1.
DR	SMART; SM00327; VWA; 1.	DR	SMART; SM00327; VWA; 1.
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.	DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR	PROSITE; PS0234; VWEA; 1.	DR	PROSITE; PS0234; VWEA; 1.
KW	Cell adhesion; Integrin; Transmembrane.	KW	Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
SQ	SEQUENCE 1151 AA; 126943 MW; 8785695D4074CA5 CRC64;	FT	SIGNAL 1 19 Potential.
Query Match			
Best Local Similarity 72.6%; Score 669; DB 2; Length 1151;			
Matches 130; Conservative 21; Mismatches 25; Indels 0; Gaps 0;			
QY	1 CPQESDIAFLIDGSGSIIPHDPRMKFVSTVMEOLKSKTLFSLMOYSEFRHFTPK 60	FT	CHAIN 20 1161 Integrin alpha-D.
Db	144 CPQESNIAFLIDGSGSINTIDFQKMKFVSTVMDQFKSKTLFSLMOYSDSFRTHFTN 203	FT	DOMAIN 20 1100 Extracellular (Potential).
QY	61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120	FT	TRANSMEM 1101 1121 Potential.
Db	204 DFKRNPDPKSHVRPIQLNGRTKSGIRKVVRELFQKNGARDNAAKILVITDGEKFG 263	FT	DOMAIN 1122 1161 Cytoplasmic (Potential).
QY	121 DPLGYEDVTEADREGVIRYVIGVDAPRSEKROELNTIASKPPRDHVFQCNNE 176	FT	REPEAT 34 87 FG-GAP 1.
Db	264 DELNYEDVTEAEAGIIRYVIGVGNFNAFKPQSRRELDTIASKPGADHVFQVDNE 319	FT	REPEAT 88 2 ? FG-GAP 2.
RESULT 5			
ID	ITAD_RAT	FT	DOMAIN 152 334 VWEA.
ID	ITAD_HUMAN	FT	REPEAT 352 402 FG-GAP 3.
AC	Q90E7.	FT	REPEAT 403 454 FG-GAP 4.
DT	05-JUL-2004 (Rel. 44, Created)	FT	REPEAT 456 517 FG-GAP 5.
DT	05-JUL-2004 (Rel. 44, Last sequence update)	FT	REPEAT 519 577 FG-GAP 6.
DT	05-JUL-2004 (Rel. 44, Last annotation update)	FT	REPEAT 582 634 FG-GAP 7.
DE	Integrin alpha-D precursor.	FT	CA_BIND 467 475 Potential.
OS	Name=Itgad;	FT	CA_BIND 531 539 Potential.
OC	Rattus norvegicus (Rat).	FT	SITE 1126 1130 GFPR motif.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	DISULFID 69 76 By similarity.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	FT	DISULFID 108 126 By similarity.
OX	NCBI_TaxID=10116;	FT	DISULFID 656 711 By similarity.
RN	[1]	FT	DISULFID 769 775 By similarity.
RP	SEQUENCE FROM N.A.	FT	DISULFID 845 860 By similarity.
RC	STRAIN=Sprague-Dawley;	FT	DISULFID 993 1017 By similarity.
RA	O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,	FT	DISULFID 1022 1027 By similarity.
RA	Gallatin W.M.;	FT	CARBOHYD 61 61 N-linked (GlcNAc..?) (Potential).
RA	"Cloning of rat alpha D, a novel beta 2 integrin.";	FT	CARBOHYD 89 89 N-linked (GlcNAc..?) (Potential).
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	FT	CARBOHYD 245 245 N-linked (GlcNAc..?) (Potential).
CC	- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and	FT	CARBOHYD 393 393 N-linked (GlcNAc..?) (Potential).
CC	VCAM1. May play a role in the atherosclerotic process such as	FT	CARBOHYD 696 696 N-linked (GlcNAc..?) (Potential).
CC	clearing lipoproteins from plaques and in phagocytosis of blood-	FT	CARBOHYD 734 734 N-linked (GlcNAc..?) (Potential).
CC	borne pathogens, particulate matter, and senescent erythrocytes	FT	CARBOHYD 784 784 N-linked (GlcNAc..?) (Potential).
CC	from the blood (By similarity).	FT	CARBOHYD 907 907 N-linked (GlcNAc..?) (Potential).
CC	- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D	FT	CARBOHYD 936 936 N-linked (GlcNAc..?) (Potential).
CC	associates with beta-2 (By similarity).	FT	CARBOHYD 1045 1045 N-linked (GlcNAc..?) (Potential).
CC	- SURCELLULAR LOCATION: Type I membrane protein (By similarity).	SQ	SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;
CC	- DOMAIN: The integrin I-domain (insert) is a VWEA domain. Integrins	Query Match	
CC	with I-domains do not undergo protease cleavage.	Best Local Similarity 59.7%; Score 550; DB 1; Length 1161;	
CC	- SIMILARITY: Belongs to the integrin alpha chain family.	Matches 106; Conservative 27; Mismatches 42; Indels 0; Gaps 0;	
CC	- SIMILARITY: Contains 7 FG-GAP repeats.	QY	1 CPQESDIAFLIDGSGSIIPHDPRMKFVSTVMEOLKSKTLFSLMOYSEFRHFTPK 60
CC	- SIMILARITY: Contains 1 VWEA domain.	Db	146 CDRQEMDIAFLIDGSGSINQDRDFAQMKDPVKALMGEPASTSLFSLMQSLNLTHTFTT 205
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	QY	61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	Db	206 EFKNLDLPQSLVDPIVQLQGLTYTATGIRTVMEELFHSKNGSKSAKKILLVITDQKYR 265
CC	the European Bioinformatics Institute. There are no restrictions on its	QY	121 DPLGYEDVTEADREGVIRYVIGVDAPRSEKROELNTIASKPPRDHVFQCNNE 175
CC	use by non-profit institutions as long as its content is in no way	Db	266 DPLEYSDVIPAADKAGIIRYVIGVDGDFQEPALKELTIGSAPPQDHVFKGVNF 320
CC	modified and this statement is not removed. Usage by and for commercial	RESULT 6	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	ITAD_HUMAN	
CC	or send an email to license@isb-sib.ch).	ID	ITAD_HUMAN
CC		AC	Q13349; Q15575; Q15576; PRT; 1162 AA.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (LeukoIntegrin alpha D) (CD11d) (ADB2).
Name=ITGAD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=96111956; PubMed=8777714;
RA Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
ST Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RX MEDLINE=20187620; PubMed=10722744;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin
gene CD11d. Essential role of Sp1 and Sp3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=9257236; PubMed=8666289;
RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene-encoding a human
beta 2-integrin alpha subunit.";
RL Gene 171:291-294(1996).
RN [4]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alpha2beta2 integrin is expressed on human eosinophils and functions
as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
1)." ;
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
binding interface between I domain and VCAM-1." ;
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
lines and subsets of peripheral blood leukocytes and strongly on
tissue-specialized cells, including macrophages foam cells within
atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (inset) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.

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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

CC EMBL; U37028; AAB38547.1; --
CC EMBL; U40274; AAB60634.1; --
CC EMBL; U40275; AAB60635.1; --
CC EMBL; U40276; AAB60636.1; --
CC EMBL; U40277; AAB60637.1; --
CC EMBL; U40279; AAB60638.1; --
CC EMBL; U40278; AAB60638.1; JOINED.
CC EMBL; AF187881; AAF62875.1; --
CC HSSP; FI1215; 1BHQ.
CC GO; HGNC:6146; ITGAD.
CC MIM; 602453; --
CC GO; GO:0008305; C:integrin complex; TAS.
CC GO; GO:0016337; P:cell-cell adhesion; NAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR000413; Integrin_alpha.
CC InterPro; IPR002035; VWFA.
CC Pfam; PF01839; FG-GAP; 3.
CC Pfam; PF00357; Integrin_alpha; 1.
CC Pfam; PF00092; VWFA; 1.
CC PRINTS; PR01185; INTEGRINA.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00191; Int_alpha; 5.
CC SMART; SM00327; VWFA; 1.
CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE; PS0234; VWFA; 1.
CC Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 1162 Integrin alpha-D.
FT DOMAIN 18 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1162 Cytoplasmic (Potential).
FT REPEAT 32 85 FG-GAP 1.
FT REPEAT 86 87 FG-GAP 2.
FT DOMAIN 150 332 VWFA.
FT REPEAT 350 400 FG-GAP 3.
FT REPEAT 401 452 FG-GAP 4.
FT REPEAT 454 516 FG-GAP 5.
FT REPEAT 518 576 FG-GAP 6.
FT REPEAT 581 633 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 530 538 Potential.
FT CA_BIND 593 601 Potential.
FT SITE 1127 1131 GFFKR motif.
FT DISULFID 67 74 By similarity.
FT DISULFID 106 124 By similarity.
FT DISULFID 655 710 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 846 861 By similarity.
FT DISULFID 994 1018 By similarity.
FT DISULFID 1023 1028 By similarity.
FT CARBOHYD 59 59 N-linked (GlcNAc...)
FT CARBOHYD 87 87 N-linked (GlcNAc...)
FT CARBOHYD 99 99 N-linked (GlcNAc...)
FT CARBOHYD 391 391 N-linked (GlcNAc...)
FT CARBOHYD 691 691 N-linked (GlcNAc...)
FT CARBOHYD 733 733 N-linked (GlcNAc...)
FT CARBOHYD 873 873 N-linked (GlcNAc...)
FT CARBOHYD 957 957 N-linked (GlcNAc...)
FT CARBOHYD 1046 1046 N-linked (GlcNAc...)
FT CONFLICT 500 500 Missing (in Ref. 2).
FT CONFLICT 515 518 GHPW -> ATP (in Ref. 2).
FT CONFLICT 825 825 L -> V (in Ref. 2).
FT CONFLICT 984 984 V -> A (in Ref. 2).
CC SEQUENCE 1162 AA; 126885 MW; F296A1A35455D77D CRC64;
Query Match 59.1%; Score 545; DB 1; Length 1162;
Best Local Similarity 60.0%; Pred. No. 7.5e-37;
Matches 105; Conservative 29; Mismatches 41; Indels 0; Gaps 0;

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QY 1 CQEDSDIAFLIDGSGSIIPHPRRMKEFVSTVMEQLKKSKTLFSLMQYSEBFRHPTFK 60
DB 144 CQEDMDIVFLIDGSGSIDQDNFNQMGFQVQVMOGFEQDTLFLALMOYSLNLLKHFTFT 203
QY 61 BFQNNPNRSLVKPTQLLGRHTTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 QRTSPSQSLVDPVQLKGLTFTAGILTVTQVLFHHKNGARKNAFKILVITDGEKRYK 263
QY 121 DPLGVEDVPEADREGVIRYVGVGDAFRSEKSRQELNTIASKPRDRHVFQCNFF 175
DB 264 DPLEYSDVIPAQEKAGILIRYAGVGHAFQGPARTARQELNTIASSAPPQDHVFKVDNF 318

RESULT 7
Q63001 PRELIMINARY; PRT; 205 AA.
AC Q63001;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Integrin alpha-M (Fragment).
GN Name=Itgam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar Kyoto;
RA Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,
RA Julier C., Maeda J., Yamori Y., Nara Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59801; AAB03226.1; -
DR GO; GO:0007229; P:intrigued-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS02334; VWPA; 1.
KW Integrin.
FT NON_TER 1
FT NON_TER 205
SQ SEQUENCE 205 AA; 22922 MW; C8C2D9395008DA36 CRC64;

Query Match 57.8%; Score 533; DB 2; Length 205;
Best Local Similarity 74.1%; Pred. No. 1,1e-36;
Matches 109; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 30 VSTVMEQLKKSKTLFSLMQYSEBFRHPTFKFQNNPNRSLVKPTQLLGRHTTATGIR 89
DB 1 VSTVMEQFQSKTLFSLMQYSDFRTHFTFNFKRNPDPKSHVRPIQLNGRTKTASGIR 60
QY 90 KVVRELFNITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVGVGDAFR 149
DB 61 KVVRELFQKNGARNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVGVGNAPF 120
QY 150 SEKSRQELNTIASKPRDRHVFQCNFF 176
DB 121 KQSRRELDITASKPAGDHVQVDNFE 147

RESULT 8
ITAX HUMAN
ID ITAX HUMAN STANDARD; PRT; 1163 AA.
AC P20702; O81VA6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Lew M5).
GN Name=ITGAX; Synonyms=CD11c;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=88166645; PubMed=3327687;
RA Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
RT "cDNA cloning and complete primary structure of the alpha subunit of a
RT leukocyte adhesion glycoprotein, p150,95."
RL EMBO J. 6:4023-4028(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153906; PubMed=2303426;
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RT "Genomic structure of an integrin alpha subunit, the leukocyte p150,95
RT molecule."
RL J. Biol. Chem. 265:2782-2788(1990).
RN [3]
RP ERRATUM.
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RL J. Biol. Chem. 265:12750-12751(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 20-43.
RX MEDLINE=87167596; PubMed=3549901;
RA Miller L.J., Wiebe M., Springer T.A.;
RT "Purification and alpha subunit N-terminal sequences of human Mac-1
RT and p150,95 leukocyte adhesion proteins."
RL J. Immunol. 138:2381-2383(1987).
CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC interaction during inflammatory responses. It is especially
CC important in monocyte adhesion and chemotaxis.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWA domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdlc entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdlc.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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DR EMBL; M81695; AAA59180.1; -;
DR EMBL; M29185; -; NOT ANNOTATED CDS.
DR EMBL; M29487; AAA51620.1; ALT_SEQ.
DR EMBL; M29482; AAA51620.1; JOINED.
DR EMBL; M29483; AAA51620.1; JOINED.
DR EMBL; M29484; AAA51620.1; JOINED.
DR EMBL; M29485; AAA51620.1; JOINED.
DR EMBL; M29486; AAA51620.1; JOINED.
DR EMBL; BC038237; AAH38237.1; -;
DR PIR; A36584; RWHUIC.
DR PDB; 1N3Y; X-ray; A=141-338.
DR Genew; HGNC:6152; ITGAX.
DR MIM; 151510; -;
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0009887; P:organogenesis; TAS.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA_1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1163
FT DOMAIN 20 1107 Integrin alpha-X.
FT TRANSMEM 1108 1128 Extracellular (Potential).
FT DOMAIN 1129 1163 Potential.
FT REPEAT 34 87 Cytoplasmic (Potential).
FT REPEAT 88 ? FG-GAP 1.
FT DOMAIN 165 351 FG-GAP 2.
FT REPEAT ? 401 VWFA.
FT REPEAT 402 453 FG-GAP 3.
FT REPEAT 455 517 FG-GAP 4.
FT REPEAT 518 576 FG-GAP 5.
FT REPEAT 581 633 FG-GAP 6.
FT CA_BIND 456 474 FG-GAP 7.
FT CA_BIND 530 538 Potential.
FT SITE 593 601 Potential.
FT SITE 1131 1135 GFPR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 655 712 By similarity.
FT DISULFID 771 777 By similarity.
FT DISULFID 848 863 By similarity.
FT DISULFID 998 1022 By similarity.
FT DISULFID 1027 1032 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 392 392 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 697 697 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 939 939 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1050 1050 N-linked (GlcNAc...) (Potential).
FT VARIANT 48 48 W -> R (in dbSNP:11574633).
FT CONFLICT 209 209 /FTID=VAR_018672.
FT CONFLICT 251 251 T -> S (in Ref. 4).
FT CONFLICT 469 469 T -> A (in Ref. 4).
FT CONFLICT 490 490 G -> S (in Ref. 4).
FT CONFLICT 547 547 T -> A (in Ref. 2).
FT CONFLICT 547 547 E -> K (in Ref. 4).

756 756 756
819 819 819
1163 1163 1163
150 150 150
161 161 161
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SQ SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DE8F CRC64;
Query Match 52.7%; Score 486; DB 1; Length 1163;
Best Local Similarity 53.4%; Pred. No. 6.6e-32;
Matches 94; Conservative 33; Mismatches 49; Indels 0; Gaps 0;
QY 1 CPQDSDFIAFLDGGSGSIIPHDFRRMKFEFVSTVMEQLKSKTFLSLMOYSEEFRIHTFK 60
Db 145 CPQEDIVFLDGGSGSISSRNFMNFVRAVTSQFQSTQSLMQFSNKFQHTFTE 204
QY 61 EFQNNPNRSLVKPTQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 205 EFRRTSNPLSLASVHQLQGFTYTATAIQNVVHFLPHASYGARDATKILIVITDGKKEG 264
QY 121 DPLGYEDVIPADREGVIRVIGVDAPRSEKSRQELNTASKPRDHVFCNNFE 176
Db 265 DSLDYKDVIPWADAAGIIRYAIGVGLAFQNNRNSWKELNDIASKPSQBHFVKVEDFD 320
RESULT 9
Q6KAS4 PRELIMINARY; PRT; 1188 AA.
ID Q6KAS4
AC Q6KAS4;
DC 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MFLJ00114 protein (Fragment).
GN Name=mrLJ00114;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikura R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Soga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).


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FT REPEAT ? 402 FG-GAP 3.
FT REPEAT 403 454 FG-GAP 4.
FT REPEAT 456 518 FG-GAP 5.
FT REPEAT 519 577 FG-GAP 6.
FT REPEAT 582 634 FG-GAP 7.
FT CA_BIND 467 475 Potential.
FT CA_BIND 531 539 Potential.
FT CA_BIND 594 602 Potential.
FT SITE 1140 1144 GFPR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 770 776 By similarity.
FT DISULFID 858 873 By similarity.
FT DISULFID 1007 1031 By similarity.
FT DISULFID 1036 1041 By similarity.
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 949 949 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1059 1059 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1084 1084 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;

Query Match 52.3%; Score 482; DB 1; Length 1169;
Best Local Similarity 52.8%; Pred. No. 1.4e-31;
Matches 93; Conservative 30; Mismatches 53; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTMQKSKTKLFLSLMQYSEEFRIHFTFK 60
Db 146 CPKQDQDIVFLIDGSGSISSTDFEKLDFVKAVMSQLQRPSTFRSLMQFSDFYRVHFTFN 205

QY 61 EFQNNPNRSLVKPIITQLGRHTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 206 NFISTSSPLSLGSRVQLRGYTYTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 265

QY 121 DPLGYEDVPEADREGVIRYVIGVDGDAFSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 266 DNLSDYDVPMAEASIIIRYAGVKAFYNEHSKQELKAIASMPSEHYVFSVENFD 321

RESULT 12
QPG66
ID QPG66 PRELIMINARY; PRT; 304 AA.
AC QPG66
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Integrin alpha X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-1/f1;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-1/f1;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057200; AAH57200.1; -.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Integrin.
SQ SEQUENCE 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;

Query Match 44.3%; Score 408; DB 2; Length 304;
Best Local Similarity 53.3%; Pred. No. 5.1e-26;
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTMQKSKTKLFLSLMQYSEEFRIHFTFK 60
Db 146 CPKQDQDIVFLIDGSGSISSTDFEKLDFVKAVMSQLQRPSTFRSLMQFSDFYRVHFTFN 205

QY 61 EFQNNPNRSLVKPIITQLGRHTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 206 NFISTSSPLSLGSRVQLRGYTYTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 265

QY 121 DPLGYEDVPEADREGVIRYVIGVG--DAF 148
Db 266 DNLSDYDVPMAEASIIIRYAGVKHKGDF 295

RESULT 13
AAH57200
ID AAH57200 PRELIMINARY; PRT; 304 AA.
AC AAH57200;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Integrin alpha X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-1/f1;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Abramson R.D., Mullaly S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057200; AAH57200.1; -.
KW Integrin. 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;
SQ SEQUENCE 304 AA; 33404 MW; 895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;

Query Match 44.3%; Score 408; DB 2; Length 304;
Best Local Similarity 53.3%; Pred. No. 5.1e-26;
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPOEDSDIAFLIDGSGSIIPHDFRMKEFVSTWMEQLKSKTLFSLMOYSEEFRIHFTFK 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 146 CPQODQIVFLIDGSGSIISSTDFKMLDFKAVMSQLQSPRFSLMQPSDFRYRVHFTFN 205

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 NFISTSSPLSLDSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVITDGRKQG 265

QY 121 DPLGYEDVIPADREGVIRYVGVG--DAF 148
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 266 DNLSYDSVIPMAEASIIIRYAGVGHKQGF 295

RESULT 14
Q9WUF8 PRELIMINARY; PRT; 895 AA.
AC Q9WUF8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Itgae protein (Fragment).
GN Name=Itgae;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoen M.P., Arya A., Murphy E.A., Adams C.M., Strauch U.G.,
RA Agace W.W., Marsal J., Donohue J.P., Her H., Beier D.R., Olson S.,
RA Lefrancois L., Brenner M.B., Grusby M.J., Parker C.M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF133085; AAD30063.1; JOINED.
DR EMBL; AF133070; AAD30063.1; JOINED.
DR EMBL; AF133071; AAD30063.1; JOINED.
DR EMBL; AF133072; AAD30063.1; JOINED.
DR EMBL; AF133073; AAD30063.1; JOINED.
DR EMBL; AF133074; AAD30063.1; JOINED.
DR EMBL; AF133075; AAD30063.1; JOINED.
DR EMBL; AF133076; AAD30063.1; JOINED.
DR EMBL; AF133077; AAD30063.1; JOINED.
DR EMBL; AF133078; AAD30063.1; JOINED.
DR EMBL; AF133079; AAD30063.1; JOINED.
DR EMBL; AF133080; AAD30063.1; JOINED.
DR EMBL; AF133081; AAD30063.1; JOINED.
DR EMBL; AF133082; AAD30063.1; JOINED.
DR EMBL; AF133083; AAD30063.1; JOINED.
DR EMBL; AF133084; AAD30063.1; JOINED.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.

DR PROSITE; PS50234; VWFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 895
SQ SEQUENCE 895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;

Query Match 34.9%; Score 322; DB 2; Length 895;
Best Local Similarity 38.3%; Pred. No. 2.7e-18;
Matches 67; Conservative 40; Mismatches 66; Indels 2; Gaps 1;

QY 3 QEDSDIAFLIDGSGSIIPHDFRMKEFVSTWMEQL--KSKTLFSLMOYSEEFRIHFTFK 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 EDGTIAIVLDGSGSIEPSDFQAKNFISTWRNFYEKCFECNFALVQGAIVQTEFDLQ 237

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 ESRDINASLAKVQSIQVQKVEKVTASAMQHVLDNIFIPSGSRKKALKVMVLTGDDIFG 297

QY 121 DPLGYEDVIPADREGVIRYVGVDAPRSEKSRQELNTIASKPPRDHVQCNNF 175
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 DPLNLTVTIVSPKMGVVRFAIGVDGAFKNNTYRELKLIASDPKEAHTFKVTNY 352

RESULT 15
Q8BS01 PRELIMINARY; PRT; 1038 AA.
AC Q8BS01;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:AS30055J10 product: integrin, alpha E,
DE epithelial-associated, full insert sequence.
GN Name=Itgae;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=92729253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861;
```


Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	912	98.9	177	5	AAU76866	Aau76866 Human int
2	903	97.9	187	2	AAU21991	Aay21991 Human com
3	903	97.9	1152	8	ADM99589	Adm99589 Human int
4	903	97.9	1152	8	ADP12435	Adp12435 Protein e
5	903	97.9	1153	2	AAAR04136	Aar04136 Alpha sub
6	903	97.9	1153	2	AAW65090	Aaw65090 Human bet
7	903	97.9	1153	3	AAAB07360	Aab07360 Human CDI
8	903	97.9	1153	5	AAAU80252	Aau80252 Human int
9	903	97.9	1153	5	ABG61469	Abg61469 Human bet
10	903	97.9	1153	5	AAO144428	Aao144428 Integrin
11	894	97.9	1153	7	ADD25615	Add25615 Binding d
12	894	97.0	177	5	AAU76865	Aau76865 Human int
13	893	96.9	191	5	AAU76856	Aau76856 Human int
14	893	96.9	191	5	AAU76847	Aau76847 Human int
15	871	94.5	216	4	AAAB66766	Aab66766 Amino aci
16	871	94.5	435	2	AAAR77461	Aar77461 GST-I-dom
17	683	74.1	199	5	ABB78072	Abb78072 Murine I-
18	559	60.6	413	2	AAW23065	Aaw23065 Rabbit be
19	559	60.6	413	2	AAW65107	Aaw65107 Rabbit be
20	559	60.6	413	2	AAW72839	Aaw72839 Rabbit al
21	559	60.6	413	2	AAW73348	Aaw73348 Rabbit al
22	559	60.6	413	3	AAO73737	Aao73737 Rabbit al
23	557	60.4	413	5	ABG61486	Abg61486 Rabbit Be
24	550	59.7	1151	2	AAW23059	Aaw23059 Rat beta
25	550	59.7	1151	2	AAW60001	Aaw60001 Rat alpha

all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemia-reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b deletion variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847

Sequence 177 AA;
Query Match 98.9%; Score 912; DB 5; Length 177;
Best Local Similarity 98.3%; Pred. No. 2.6e-94;
Matches 174; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 177
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 177

RESULT 2
AAV21991
ID AAV21991 standard; protein; 187 AA.
XX AAV21991;
AC AAV21991;
XX
DT 13-SEP-1999 (first entry)
DE Human complement factor MAC-1 vWF domain sequence.
XX Factor B analogue; modified; complement activity; complement factor B;
KW short consensus repeat domain; von Willebrand Factor domain; human; C2;
KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
XX
OS Homo sapiens.
XX US928892-A.
FN
XX 27-JUL-1999.
PD
XX 26-JUL-1996; 96US-00687706.
PF
XX 03-JAN-1994; 94US-00177109.
PR
XX (UNIW) UNIV WASHINGTON.
PA
XX Oglesby TJ, Hourcade DE;
PI
XX WPI; 1999-429498/36.
DR
XX Nucleic acids encoding complement protein homologues useful for
PT modulating function of the complement system in the treatment of a
PT variety of immune and autoimmune complex mediated syndromes.
XX
PS Disclosure; Fig 5A-B; S3pp; English.

XX The invention relates to a Factor B analogue that exhibits modified
CC complement activity in vitro. The analogue is generated by substituting a
CC short consensus repeat domain (SCR) or a von Willebrand Factor domain
CC (vWF) of human factor B with a SCR or a vWF from a second protein such as
CC human C2 or CR3. The analogues may be used to regulate the complement
CC system involved in immune and autoimmune responses. Complement activity
CC can account for substantial tissue damage in a wide variety of autoimmune
CC /immune complex mediated syndromes such as lupus erythematosus,
CC rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
CC of the complement system using the analogues is likely to provide a means
CC of therapeutic intervention in these cases. Inhibition of complement may
CC also be favorable in cases that involve tissue damage caused by vascular
CC injury such as myocardial infarction, cerebral vascular accidents or
CC acute shock lung syndrome. In these cases the complement system may
CC contribute to the destruction of partially damaged tissue as in
CC reperfusion injury. In addition, the use of complement analogues with
CC novel target specificities could reduce the activity of tissue damaging
CC proteins at sites of inflammation. Complement inhibition is important in
CC the prevention of xenograft rejection (the inhibition of complement by
CC cell-associated and soluble inhibitors is useful in protecting the
CC transplant from damage caused by activation of endogenous complement. The
CC present sequence represents the vWF domain of human factor MAC-1

Sequence 187 AA;
Query Match 97.9%; Score 903; DB 2; Length 187;
Best Local Similarity 99.4%; Pred. No. 2.9e-93;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 176
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 176

RESULT 3
ADM99589
ID ADM99589 standard; protein; 1152 AA.
XX ADM99589;
AC ADM99589;
XX 17-JUN-2004 (first entry)
DT Human integrin alphaM subunit precursor protein.
DE
XX integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
KW osteopathic; cytostatic; immunosuppressive; anti-inflammatory;
KW neuroprotective; antiskinning; immunotherapy; inflammatory;
KW autoimmune disorder; thrombosis; cancer; osteoporosis;
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
KW alphasM.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key
FT Misc-difference 965 /note= "Encoded by CCC"
XX
XX WO2004007530-A2.
FN
XX 22-JAN-2004.
PD
XX 17-JUL-2003; 2003WO-US022301.
PF
XX 17-JUL-2002; 2002US-0396783P.
PR

PR 17-JUL-2002; 2002US-0396790P.
PR 11-SEP-2002; 2002US-0410135P.
XX (BLOO-) CENT BLOOD RES INC.
XX Springer TA, Takagi J;
XX WPI; 2004-122877/12.
DR N-PSDB; ADM95588.
XX Novel modified integrin protein having extracellular domains of integrin
PT alpha and beta subunits or integrin alphaII and beta3 subunit, useful for
PT treating integrin mediated disorders.
XX
XX Disclosure; SEQ ID NO 4; 232pp; English.
XX The invention relates to a novel isolated or recombinant modified
CC integrin protein having extracellular domains of integrin alpha and beta
CC subunits where one of the subunits has one or more mutations, an altered
CC surface feature or an amino acid substitution or internal deletion,
CC extracellular domains of the integrin beta subunit that comprise a
CC mutation that alters a non-cysteine residue to cysteine or extracellular
CC domains of integrin alpha and beta subunits. The polypeptide of the
CC invention demonstrates antipruritic, thrombolytic, anticoagulant,
CC osteopathic, cytostatic, immunosuppressive, antiinflammatory,
CC neuroprotective and antisickling activities and may be useful for
CC immunotherapy in order to prevent or treat an integrin-mediated disorder
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
CC sclerosis. The current sequence is that of the human integrin alpha
CC subunit precursor protein of the invention.
XX
XX SQ Sequence 1152 AA;
Query Match 97.9%; Score 903; DB 8; Length 1152;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTEK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTEK 203
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319
RESULT 4
ADP12435
ID ADP12435 standard; protein; 1152 AA.
XX
XX AC ADP12435;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Protein encoded by mRNA of the invention #45.
XX
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX OS Homo sapiens.
XX
XX PN WO2004042346-A2.
XX
XX PD 21-MAY-2004.
XX
XX PF 24-APR-2003; 2003WO-US012946.
XX
XX PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX PS Claim 65; SEQ ID NO 2444; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
XX SQ Sequence 1152 AA;
Query Match 97.9%; Score 903; DB 8; Length 1152;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTEK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTEK 203
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319
RESULT 5
AAR04136
ID AAR04136 standard; protein; 1153 AA.
XX
XX AC AAR04136;
XX
XX DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 07-SEP-1990 (first entry)
XX
XX DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
XX
XX KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
KW non-specific defence system; integrin gene superfamily.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Region 1..16
FT Modified-site /label= signal_peptide
FT Modified-site 86..88
FT Modified-site /label= putative N-glycosylation site
FT Modified-site 240..242
FT Modified-site /label= putative N-glycosylation site

FT Modified-site 391..393
/label= putative N-glycosylation site
FT Modified-site 469..471
/label= putative N-glycosylation site
FT Modified-site 693..695
/label= putative N-glycosylation site
FT Modified-site 697..699
/label= putative N-glycosylation site
FT Modified-site 735..737
/label= putative N-glycosylation site
FT Modified-site 802..804
/label= putative N-glycosylation site
FT Modified-site 881..883
/label= putative N-glycosylation site
FT Modified-site 901..903
/label= putative N-glycosylation site
FT Modified-site 912..914
/label= putative N-glycosylation site
FT Modified-site 941..943
/label= putative N-glycosylation site
FT Modified-site 947..949
/label= putative N-glycosylation site
FT Modified-site 979..981
/label= putative N-glycosylation site
FT Modified-site 994..996
/label= putative N-glycosylation site
FT Modified-site 1022..1024
/label= putative N-glycosylation site
FT Modified-site 1045..1047
/label= putative N-glycosylation site
FT Modified-site 1051..1053
/label= putative N-glycosylation site
FT Modified-site 1076..1078
/label= putative N-glycosylation site
FT Modified-site 1106..1134
/label= putative transmembrane_region
FT Region
XX EP364690-A.
PN
XX
XX 25-APR-1990.
XX
XX 17-AUG-1989; 89EP-00115159.
XX
XX 23-AUG-1988; 88US-00235353.
PR 09-MAR-1989; 89US-00321239.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Springer TA, Corbi A;
XX
XX WPI; 1990-125938/17.
DR N-PSDB; AAQ04043.
XX
XX New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating
inflammation and viral infections, and in diagnosis.
XX
XX Disclosure; Page ?; 3pp; English.
XX
XX Mac-1 alpha subunit is involved in the response to inflammation, i.e.
recognition of and migration to sites of inflammation. It also attaches
to cellular substrates as part of this function making it useful in
visualising endothelial tissue. Mac-1 is a member of the Integrin Gene
superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
-MAR-2003 to correct PA field.)
XX
XX Revised record issued on 09-SEP-2004 : Correction to feature table key
and pages
XX
XX Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
|
Db 144 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
|
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
|
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 263
|
QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRDRHVFQVNNFE 176
|
Db 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRDRHVFQVNNFE 319
|
RESULT 6
AAW65090
ID AAW65090 standard; protein; 1153 AA.
XX
AC AAW65090;
XX
XX 28-SEP-1998 (first entry)
XX Human Beta-integrin CD11b subunit protein.
XX Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
XX type-I diabetes; atherosclerosis; multiple sclerosis; asthma;
XX lung inflammation; acute respiratory distress syndrome; CD11b subunit;
XX rheumatoid arthritis.
XX
OS Homo sapiens.
XX
XX US5728533-A.
XX
PD 17-MAR-1998.
XX
XX 07-JUN-1995; 95US-00485618.
XX
PR 23-DEC-1993; 93US-00173497.
PR 05-AUG-1994; 94US-00286889.
PR 21-DEC-1994; 94US-00362652.
XX
XX (ICOS-) ICOS CORP.
XX
XX Van Der Vieren M, Gallatin WM;
XX
XX WPI; 1998-206565/18.
XX
XX Screening assay for modulators of integrin binding - using immobilised or
XX labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
XX
XX Example 5; Fig 1A-D; 106pp; English.
XX
XX This sequence represents a human beta-integrin CD11b subunit which is
XX used to describe a method for identifying compounds that modulate the
XX interaction of the beta-integrin alpha-d subunit with a binding partner
XX of alpha-d which involves contacting an alpha-d polypeptide with an alpha
XX -d binding partner, one of which is immobilised and the other of which is
XX labelled, in the presence of a test compound, and determining if the
XX compound affects binding between the alpha-d polypeptide and alpha-d
XX binding partner, where the alpha-d polypeptide is alpha-d or its fragment
XX comprising the cytoplasmic, transmembrane or extracellular domain of
XX alpha-d. Compounds that modulate alpha-d binding could be used to treat
XX diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
XX asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
XX and rheumatoid arthritis
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60

Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKKEFVSTVMEQLKSKTFLSLMQYSEFRHFTPK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 7
AAB07360
ID AAB07360 standard; protein; 1153 AA.
AC AAB07360;
DT 17-JAN-2001 (first entry)
XX Human CD11b protein sequence.
DE Human; macrophage infiltration inhibition; alpha d integrin;
KW leukocyte integrin; Leu-CAM; leukointegrin; immune response;
KW inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
KW atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;
KW rheumatoid arthritis; central nervous system injury; CD11b.
OS Homo sapiens.
XX
XX
PN WO200029446-A1.
XX
XX 25-MAY-2000.
PD
PF 16-NOV-1999; 99WO-US027139.
XX
XX 16-NOV-1998; 98US-00193043.
PR 08-JUL-1999; 99US-00350259.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin MW, Van Der Vieren M;
PI WPI; 2000-387751/33.
XX
XX Use of novel anti-alpha integrin d monoclonal antibodies to inhibit
PT macrophage infiltration and reduce inflammation at central nervous system
PT injury sites.
XX
XX Example 5; Fig 1; 270pp; English.
XX
XX Integrins are a class of membrane-associated molecules that participate
CC in cellular adhesion. Integrins are made up of an alpha subunit and a
CC beta subunit. One class of human integrins are restricted to expression
CC in white blood cells and have a common beta2 subunit: the leukocyte
CC integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins
CC have an important role in immune and inflammatory responses. The present
CC protein sequence is the human integrin alpha subunit CD11b. This sequence
CC was used in an alignment to identify a novel beta2 integrin alpha
CC subunit: alpha_d (AAK60014 and AAB07359). The present sequence has
CC approximately 60% identity to the protein sequence of alpha_d. The
CC Alpha_d gene and protein may be useful in therapy for diseases linked to
CC aberrant alpha_d function e.g. Type I diabetes, atherosclerosis, multiple
CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory
CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency
CC (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
CC inhibition of macrophage infiltration at the site of a central nervous
CC system injury. The monoclonal antibodies can also be used to detect and
CC diagnose Crohn's disease
XX
XX Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 3; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKKEFVSTVMEQLKSKTFLSLMQYSEFRHFTPK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKKEFVSTVMEQLKSKTFLSLMQYSEFRHFTPK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 8
AAB08252
ID AAB08252 standard; protein; 1153 AA.
AC AAB08252;
DT 15-JUL-2002 (first entry)
XX Human integrin 1 alpha-M subunit protein.
DE Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;
KW inflammatory disease; autoimmune disorder; Crohn's disease;
KW human immunodeficiency virus; HIV; myocardial infarction;
KW Sjorgen's syndrome; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 499..500 /note= "Encoded by GGG CAG AGG"
FT
XX
PN WO200218583-A2.
XX
PD 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027227.
PF
PR 01-SEP-2000; 2000US-0229700P.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
XX Springer TA, Shimoaka M, Lu C;
PI
XX
XX WPI; 2002-382964/41.
DR N-PSDB; ABK50046.
XX
XX Modified integrin-I or integrin I-like domain polypeptide useful as an
PT immunogen to produce antibodies specific to polypeptide, comprises a
PT disulfide bond such that polypeptide is stabilized in a desired
PT conformation.
XX
PS Disclosure; Page 109-112; 112pp; English.
XX
CC This invention relates to a modified integrin-I or integrin I-like domain
CC polypeptide comprising at least one disulfide bond so that the domain is
CC stabilised in a desired conformation. The polypeptide of the invention
CC may have antiinflammatory or immunosuppressive activities. The
CC polypeptides of the invention have an open conformation and are useful as
CC immunogens to produce antibodies that selectively bind to integrin I-
CC domain; and for identifying a modulator of integrin activity, or of
CC interaction of an integrin and a cognate ligand. The polypeptide of the
CC invention, or antibodies (preferably anti-LFA-1 antibody) is useful for
CC treating or preventing an integrin mediated disorder which is an
CC inflammatory or autoimmune disorder in a subject and for inhibiting the
CC binding of an integrin to a cognate ligand such as Crohn's disease,
CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,

CC Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
CC composition comprising the peptide of the invention is useful for
CC treating an integrin mediated disorder in a subject. The polypeptides
CC and/or active or antigenic fragments are useful as reagents for diagnosis
CC of integrin-mediated disorders. The present sequence represents the human
CC integrin-1 alpha-M protein subunit used to generate the mutant
CC polypeptides of the invention
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 5; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 9
ID ABG61469
XX ABG61469 standard; protein; 1153 AA.
AC ABG61469;
DT 27-AUG-2002 (first entry)
XX
XX Human Beta2 integrin alphaCD11b subunit.
DE Beta2 integrin; alphaD subunit; CD11c subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
XX
OS Homo sapiens.
XX
XX WO200230980-A2.
XX
PD 18-APR-2002.
XX
PF 15-OCT-2001; 2001WO-US032059.
XX
XX 13-OCT-2000; 2000US-00688307.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gallatin WM, Van Der Vieren M;
XX
DR WPI; 2002-463260/49.
XX
PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
PT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
PT limiting autonomic and sensory dysfunction following spinal cord injury.
XX
XX Example 5; Page 191-194; 270pp; English.

PS The invention relates to promoting locomotor recovery, inhibiting
CC locomotor damage, limiting locomotor impairment, or limiting autonomic
CC and sensory dysfunction following spinal cord injury by administering an
CC anti-alpha_d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
CC spinal cord injury victim. The method also involves the use of a ligand

CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
CC vascular cell adhesion molecule). The method is useful for promoting
CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
CC impairment, or limiting autonomic and sensory dysfunction following
CC spinal cord injury. In particular, the spinal cord injury comprises
CC compression of the spinal cord. The antibodies are also useful for
CC reducing inflammation at the site of a central nervous system injury. The
CC specification also details the identification of Beta2 integrin alphaD
CC cDNAs and proteins, for use in raising the antibodies. Beta2 integrins
CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
CC colitis, immune complex alveolitis and leukaemia. The present sequence is
CC a Beta2 integrin alpha subunit sequence included for comparison with the
CC Beta2 integrin alphaD protein sequences
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 5; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 10
AAO14428
ID AAO14428 standard; protein; 1153 AA.
XX
AC AAO14428;
XX
DT 03-MAY-2002 (first entry)
XX
DE Integrin Mac-1 alpha subunit.
XX
KW Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
KW open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.
XX
OS Unidentified.
XX
XX WO200204521-A2.
XX
XX 17-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021805.
XX
XX 07-JUL-2000; 2000US-0216600P.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
PA (BLOO-) CENT BLOOD RES.
XX
PI Springer T;
XX
XX WPI; 2002-148167/19.
XX
PT New integrin I domain protein having alteration in at least 2
PT noncontiguous regions and exits in an open conformation, useful for
PT treating, preventing or suppressing inflammatory or immunological
PT disorders.

XX Example 1; Fig 1F; 90pp; English.

XX The invention comprises structurally biased variant integrin inserted (I)

CC domain proteins, wherein the alterations to the protein occur in at least

CC two noncontinuous regions. Specifically the variant integrin I domain

CC proteins are structurally biased to exist in the open conformation,

CC thereby altering the binding ability of the protein. The invention also

CC comprises nucleic acids encoding the variant integrin I domain proteins.

CC The integrin I domain proteins and nucleic acids are useful for treating,

CC preventing or suppressing integrin related inflammatory and immunological

CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain

CC proteins and nucleic acids can also be used for treating: ischaemia/

CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral

CC infection; and cancer. The variant integrin I domain nucleic acids and

CC proteins may be used in gene therapy, as vaccines and to screen for

CC bioactive agents. The present amino acid sequence represents the Mac-1

CC alpha subunit of integrin

XX Sequence 1153 AA;

SQ

Query Match 97.9%; Score 903; DB 5; Length 1153;

Best Local Similarity 99.4%; Pred No. 3.7e-92;

Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60

DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176

DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 11

ID ADD25615

XX ADD25615 standard; protein; 1153 AA.

AC ADD25615;

XX 15-JAN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated protein #85.

XX Binding domain; immunoglobulin; fusion protein; cytostatic;

KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;

KW neuroprotective; hinge region; immunoglobulin heavy chain;

KW CH2 constant region; CH3 constant region; IgG1;

KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;

KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;

KW rheumatoid arthritis; myasthenia gravis; Grave's disease;

KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

XX US2003118592-A1.

PN 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

PF 17-JAN-2001; 2001US-0367358P.

PR 17-JAN-2002; 2002US-00053530.

PR 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENE-CRAFT INC.

PA Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX

DR WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

PT subject having or suspected of having a malignant condition or a B-cell

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

XX

PS Disclosure; SEQ ID NO 176; 157pp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein

CC comprising a binding domain polypeptide that is fused to an

CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain

CC CH2 constant region polypeptide that is fused to the hinge region

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region

CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin

CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge

CC region polypeptide; derived from (a) having 3 or more cysteine residues;

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide

CC contains 2 cysteine residues, where the first cysteine is not mutated; a

CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from

CC (a) having 3 or more cysteine residues, where the mutated human IgG1

CC immunoglobulin hinge region polypeptide contains no more than one

CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region

CC polypeptide, derived from (a) having 3 or more cysteine residues; where

CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody

CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The

CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the

CC binding domain-immunoglobulin fusion protein, a recombinant expression

CC construct comprising the polynucleotide (operably linked to a promoter),

CC a host cell transformed or transfected with a recombinant expression

CC construct, producing the binding domain-immunoglobulin fusion protein, a

CC pharmaceutical composition comprising the binding domain-immunoglobulin

CC fusion protein or polynucleotide and a carrier, and treating a subject

CC having or suspected of having a malignant condition or a B-cell disorder.

CC The binding domain-immunoglobulin fusion protein is useful for treating a

CC subject having or suspected of having a malignant condition or a B-cell

CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,

CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple

CC sclerosis or autoimmune disease. The present sequence is a binding domain

CC -immunoglobulin fusion protein-associated protein sequence. Note: The

CC sequence data for this patent formed part of the printed specification

CC and is also available in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not

CC identified the sequences in the printed specification by their SEQ ID

CC number therefore none of the sequences can be explicitly identified.

XX

SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 7; Length 1153;

Best Local Similarity 99.4%; Pred No. 3.7e-92;

Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60

DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176

DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 12

AAU76865

ID AAU76865 standard; protein; 177 AA.

XX

AC AAU76865;

Best Local Similarity 97.7%; Pred. No. 4e-92; Mismatches 2; Indels 0; Gaps 0;
Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLLVLTGDKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLLVLTGDKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 14
AAU76847
ID AAU76847 standard; protein; 191 AA.
XX
AC AAU76847;
DT 21-MAY-2002 (first entry)
DE Human integrin alpha subunit CD11b A domain.
XX
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..188
FT /note="This region is specifically claimed"
XX
PN WO200209737-A1.
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023957.
XX
PR 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Arnaut AM, Li R, Xiong J;
XX
DR WPI; 2002-188687/24.
XX
PT Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
PS Example 2; Fig 5; 55pp; English.
XX
CC The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents the human

CC integrin alpha subunit CD11b A domain
XX
SQ Sequence 191 AA;
Query Match 96.9%; Score 893; DB 5; Length 191;
Best Local Similarity 97.7%; Pred. No. 4e-92; Mismatches 2; Indels 0; Gaps 0;
Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLLVLTGDKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLLVLTGDKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 15
AAB66766
ID AAB66766 standard; protein; 216 AA.
XX
AC AAB66766;
DT 10-APR-2001 (first entry)
DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
XX
KW EST; expressed sequence tag; inclusion body; binding partner;
KW immunoglobulins.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200102588-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-EP006137.
XX
PR 02-JUL-1999; 99EP-00112815.
XX
PA (MORP-) MORPHOSYS AG.
XX
PI Friesch C, Kretzschmar T, Hoess A, Von Rueden T;
XX
DR WPI; 2001-147085/15.
XX
PT Generating specific binding partners to (poly)peptides encoded by genomic
PT DNA fragments, involves forming inclusion bodies by expressing the
PT (poly)peptide as part of fusion proteins.
XX
PS Disclosure; Page 18; 45pp; English.
XX
CC The present invention relates to generating a specific binding partner to
CC a peptide, encoded by a genomic DNA fragment or an expressed sequence tag
CC (EST). A nucleic acid molecule encoding a fusion protein is expressed in
CC a host cell to allow the formation of inclusion bodies comprising the
CC fusion protein, the inclusion bodies are isolated and a specific binding
CC partner is generated. The specific binding partners generated are useful
CC for identifying and characterizing naturally occurring proteins e.g. as
CC immunoglobulins or fragments in immunoassays
XX
SQ Sequence 216 AA;
Query Match 94.5%; Score 871; DB 4; Length 216;
Best Local Similarity 99.4%; Pred. No. 1.4e-89;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQNN 65

Db	12	SDIAFLIDGSGSII PHDFREMKFVSTVMEQLKSKTLP SLMQYSEEFRIHFTTFKFOQN	71
Qy	66	PNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLCY	125
Db	72	PNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLCY	131
Qy	126	EDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE	176
Db	132	EDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE	182

Search completed: January 13, 2005, 15:12:33
Job time : 34.0928 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2005, 15:13:36 ; Search time 29.2475 Seconds
(without alignments)
2186.449 Million cell updates/sec

Title: RWHULB-C_COPY_144_320

Perfect score: 922

Sequence: 1 CPQEDSDIAFLIDGSGSIIP.....NTIASKPPRDHVFQCNNEC 177

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	903	97.9	191	10	US-09-805-354-1
2	903	97.9	191	11	US-09-758-493-1
3	903	97.9	191	14	US-10-144-259-1
4	903	97.9	1152	9	US-09-945-265-4
5	903	97.9	1153	9	US-09-350-259-3
6	903	97.9	1153	10	US-09-902-481A-1
7	903	97.9	1153	10	US-09-891-943-3
8	903	97.9	1153	14	US-10-144-259-30
9	903	97.9	1153	14	US-10-207-655-176
10	894	97.0	1137	10	US-09-902-481A-6
11	889	96.4	1137	10	US-09-902-481A-5
12	879	95.3	1137	10	US-09-902-481A-4
13	877	95.1	184	15	US-10-346-863-17

14	877	95.1	187	15	US-10-346-863-37	Sequence 37, Appl
15	877	95.1	187	16	US-10-615-515-9	Sequence 9, Appl
16	871	94.5	190	15	US-10-346-863-42	Sequence 42, Appl
17	871	94.5	190	15	US-10-346-863-48	Sequence 48, Appl
18	871	94.5	216	10	US-09-795-872-5	Sequence 5, Appl
19	871	94.5	216	16	US-10-662-824-5	Sequence 5, Appl
20	871	94.5	1137	10	US-09-902-481A-3	Sequence 3, Appl
21	683	74.1	199	14	US-10-066-551-11	Sequence 11, Appl
22	683	74.1	199	17	US-10-665-990A-11	Sequence 11, Appl
23	559	60.6	413	9	US-09-350-259-101	Sequence 101, App
24	559	60.6	413	10	US-09-891-943-101	Sequence 101, App
25	550	59.7	1151	9	US-09-350-259-37	Sequence 37, Appl
26	550	59.7	1151	10	US-09-891-943-37	Sequence 37, Appl
27	550	59.7	1161	9	US-09-350-259-55	Sequence 55, Appl
28	550	59.7	1161	10	US-09-891-943-55	Sequence 55, Appl
29	545	59.1	191	10	US-09-805-354-3	Sequence 3, Appl
30	545	59.1	191	11	US-09-758-493-3	Sequence 3, Appl
31	545	59.1	191	14	US-10-144-259-3	Sequence 3, Appl
32	545	59.1	1161	9	US-09-350-259-2	Sequence 2, Appl
33	545	59.1	1161	9	US-09-350-259-99	Sequence 99, Appl
34	545	59.1	1161	10	US-09-891-943-2	Sequence 2, Appl
35	545	59.1	1161	10	US-09-891-943-99	Sequence 99, Appl
36	544	59.0	1155	9	US-09-350-259-46	Sequence 46, Appl
37	544	59.0	1155	10	US-09-891-943-46	Sequence 46, Appl
38	544	59.0	1161	9	US-09-350-259-53	Sequence 53, Appl
39	544	59.0	1161	10	US-09-891-943-53	Sequence 53, Appl
40	488	52.9	1163	9	US-09-350-259-4	Sequence 4, Appl
41	488	52.9	1163	10	US-09-891-943-4	Sequence 4, Appl
42	486	52.7	191	10	US-09-805-354-2	Sequence 2, Appl
43	486	52.7	191	11	US-09-758-493-2	Sequence 2, Appl
44	486	52.7	191	14	US-10-144-259-2	Sequence 2, Appl
45	486	52.7	1163	14	US-10-116-275-204	Sequence 204, App

ALIGNMENTS

RESULT 1

US-09-805-354-1
; Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; PRIOR FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1

Query Match	97.9%	Score 903;	DB 10;	Length 191;
Best Local Similarity	99.4%	Pred. No. 6.2e-89;		
Matches 175;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	1	CPQEDSDIAFLIDGSGSIIPHD	FRMKFVSTVMOLKSKTLFSLMQYSEFRHFTFK	60
Db	1	CPQEDSDIAFLIDGSGSIIPHD	FRMKFVSTVMOLKSKTLFSLMQYSEFRHFTFK	60
Qy	61	EFQNNPNRSLVKPITQLLGRTH	TATGIRKVVRELFNITNGARKNAFKLVITDGEKFG	120
Db	61	EFQNNPNRSLVKPITQLLGRTH	TATGIRKVVRELFNITNGARKNAFKLVITDGEKFG	120

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RESULT 2

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US-09-758-493-1
; Sequence 1, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-1

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	Query Match	97.9%;	Score 903;	DB 11;	Length 191;
	Best Local Similarity	99.4%;	Pred. No. 6.2e-89;		
	Matches 175;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
Qy	1	CPQEDSDIAFLIDGGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEERFRIHPTFK	60		
Db	1	CPQEDSDIAFLIDGGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEERFRIHPTFK	60		
Qy	61	EFQNNPNRSLVKPITQLGLRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120		
Db	61	EFQNNPNRSLVKPITQLGLRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120		
Qy	121	DPUGYEDVTPADRGRVIRYIVGVGDAPRSEKSGQELNTIASKPPRDHVFQCNFFE	176		
Db	121	DPUGYEDVTPADRGRVIRYIVGVGDAPRSEKSGQELNTIASKPPRDHVFQCNFFE	176		

RESULT 3

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US-10-144-259-1
; Sequence 1, Application US/10144259
; Publication No. US2003010961A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-1

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Qy	1	CPQEDSIAFLIDGSGSIIPHDFRPMKEFVSTMQLKKSKTILFSLMQYSEFRJHFTFK	60
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Qy	61	BFQNNPNRSLVKBITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG	120
Db	61	BFQNNPNRSLVKBITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG	120
Qy	121	DPLGYEDVIEADREGVIRYVIGVDAPFRSKSQELNTIASKPPRDHVFQCNPEE	176
Db	121	DPLGYEDVIEADREGVIRYVIGVDAPFRSKSQELNTIASKPPRDHVFQCNPEE	176

RESULT 4

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US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4

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RESULT 5

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US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350, 259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363

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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match          97.9%; Score 903; DB 9; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 6
US-09-902-481A-1
; Sequence 1, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: PRT
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; LOCATION: (17)..()
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US-09-902-481A-1

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Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 7
US-09-891-943-3
; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-943-3

Query Match          97.9%; Score 903; DB 10; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFINITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 8
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-30

Query Match          97.9%; Score 903; DB 14; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSESEFRIHFTFK 203
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QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
|||
Db 204 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
|||
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 176
|||
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 319
|||

RESULT 9

US-10-207-655-176
; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-176

Query Match 97.9%; Score 903; DB 14; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
|||
Db 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
|||
QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
|||
Db 204 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
|||
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 176
|||
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 319
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RESULT 10

US-09-902-481A-6
; Sequence 6, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-6

Query Match 97.0%; Score 894; DB 10; Length 1137;
Best Local Similarity 97.2%; Pred. No. 6.7e-87;
Matches 171; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
|||
Db 128 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 187
|||
QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
|||
Db 188 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247
|||
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 176
|||
Db 248 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 303
|||

RESULT 11

US-09-902-481A-5
; Sequence 5, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-5

Query Match 96.4%; Score 889; DB 10; Length 1137;
Best Local Similarity 95.5%; Pred. No. 2.3e-86;
Matches 168; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
|||
Db 128 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 187
|||
QY 61 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
|||
Db 188 EFQNNPNRSLVKPITQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247
|||
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 176
|||
Db 248 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFOQNPE 303
|||

RESULT 12

US-09-902-481A-4
; Sequence 4, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 4
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match          95.3%; Score 879; DB 10; Length 1137;
Best Local Similarity 94.9%; Pred. No. 2.8e-85;
Matches 167; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 187
QY 61 EFQNNPNRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247
QY 121 DPLGYVEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNNE 176
DB 248 DPLGYVEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNNE 303

RESULT 13
US-10-346-863-17
; Sequence 17, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-17

Query Match          95.1%; Score 877; DB 15; Length 184;
Best Local Similarity 99.4%; Pred. No. 3.8e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

RESULT 14
US-10-346-863-37
; Sequence 37, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match          95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
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; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match          95.1%; Score 877; DB 15; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

RESULT 15
US-10-615-515-9
; Sequence 9, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-9

Query Match          95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NNPRSLVKPIITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
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Qy 125 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 121 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNPE 172

Search completed: January 13, 2005, 15:39:45
Job time : 30.2475 secs

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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 8.50625 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWULB-C_COPY_144_320
Perfect score: 922
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....NTIASKPRDRHVQCNNEC 177

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	903	97.9	187	2	US-08-177-109A-61
2	903	97.9	187	2	US-08-687-706-61
3	903	97.9	1152	2	US-08-476-062A-43
4	903	97.9	1152	5	PCT-US96-01314-43
5	903	97.9	1152	6	5424399-2
6	903	97.9	1153	1	US-08-173-497-3
7	903	97.9	1153	1	US-08-286-889-3
8	903	97.9	1153	1	US-08-485-618-3
9	903	97.9	1153	1	US-08-362-652-3
10	903	97.9	1153	2	US-08-605-672-3
11	903	97.9	1153	2	US-08-482-293A-3
12	903	97.9	1153	2	US-08-943-363-3
13	903	97.9	1153	3	US-09-193-043-3
14	903	97.9	1153	4	US-09-688-307A-3
15	903	97.9	1153	4	US-09-350-259-3
16	871	94.5	216	4	US-09-795-872-5
17	871	94.5	435	5	PCT-US95-04439-1
18	559	60.6	413	1	US-08-485-618-101
19	559	60.6	413	2	US-08-605-672-101
20	559	60.6	413	2	US-08-482-293A-101
21	559	60.6	413	2	US-08-943-363-101
22	559	60.6	413	3	US-09-193-043-101
23	559	60.6	413	4	US-09-688-307A-101
24	559	60.6	413	4	US-09-350-259-101
25	550	59.7	1151	1	US-08-286-889-37
26	550	59.7	1151	1	US-08-485-618-37
27	550	59.7	1151	1	US-08-362-652-37

28	550	59.7	1151	2	US-08-605-672-37	Sequence 37, Appl
29	550	59.7	1151	2	US-08-482-293A-37	Sequence 37, Appl
30	550	59.7	1151	2	US-08-943-363-37	Sequence 37, Appl
31	550	59.7	1151	3	US-09-193-043-37	Sequence 37, Appl
32	550	59.7	1151	4	US-09-688-307A-37	Sequence 37, Appl
33	550	59.7	1151	4	US-09-350-259-37	Sequence 37, Appl
34	550	59.7	1151	1	US-08-485-618-55	Sequence 55, Appl
35	550	59.7	1161	1	US-08-362-652-55	Sequence 55, Appl
36	550	59.7	1161	2	US-08-605-672-55	Sequence 55, Appl
37	550	59.7	1161	2	US-08-482-293A-55	Sequence 55, Appl
38	550	59.7	1161	2	US-08-943-363-55	Sequence 55, Appl
39	550	59.7	1161	3	US-09-193-043-55	Sequence 55, Appl
40	550	59.7	1161	4	US-09-688-307A-55	Sequence 55, Appl
41	550	59.7	1161	4	US-09-350-259-55	Sequence 55, Appl
42	545	59.1	1161	1	US-08-173-497-2	Sequence 2, Appl
43	545	59.1	1161	1	US-08-286-889-2	Sequence 2, Appl
44	545	59.1	1161	1	US-08-485-618-2	Sequence 2, Appl
45	545	59.1	1161	1	US-08-485-618-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-61

Query Match 97.9%; Score 903; DB 2; Length 187;
Best Local Similarity 99.4%; Pred. No. 8.9e-93;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDSGSIIPHDFFRMKBFVSVTMVQKSKTFLFSLMQYSEFRHFTFK 60
DB 1 CPQEDSDIAFLIDSGSIIPHDFFRMKBFVSVTMVQKSKTFLFSLMQYSEFRHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

Db 61 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 176
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 2

US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-687-706-61

Query Match 97.9%; Score 903; DB 2; Length 187;
Best Local Similarity 99.4%; Pred. No. 8.9e-93;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEPRIHFTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEPRIHFTFK 60
QY 61 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 176
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 3

US-08-476-062A-43
; Sequence 43, Application US/08476062A

; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-476-062A-43

Query Match 97.9%; Score 903; DB 2; Length 1152;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEPRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEPRIHFTFK 203
QY 61 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQNNFE 319
RESULT 4
PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear.
PCT-US96-01314-43

Query Match 97.9%; Score 903; DB 5; Length 1152;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 5
5424399-2
PATENT NO. 5424399
APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 212,573
FILING DATE: 28-JUN-1988
SEQ ID NO: 2
LENGTH: 1152
5424399-2

Query Match 97.9%; Score 903; DB 6; Length 1152;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 60

DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 176

DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 6

US-08-173-497-3
Sequence 3, Application US/08173497
Patent No. 5437958
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-173-497-3

Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMRKGFVSTVMEQLKSKTFLSLMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 176

DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 7


```
US-08-286-889-3
; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-3

Query Match          97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319

RESULT 8
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
```

```
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-3

Query Match          97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319

RESULT 9
US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3

Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 319

RESULT 10
US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE: 23-DEC-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match 97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 319

RESULT 11
US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE: 23-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

```
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: /Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32694
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1153 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-482-293A-3

Query Match          97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQNNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQNNPE 319

RESULT 12
US-08-943-363-3
/ Sequence 3, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1153 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-943-363-3

Query Match          97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQNNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQNNPE 319

RESULT 13
US-08-193-043-3
/ Sequence 3, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ CURRENT FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1153
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-193-043-3

Query Match          97.9%; Score 903; DB 3; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQNNPE 176
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Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
|||||

RESULT 14

US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3

Query Match 97.9%; Score 903; DB 4; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVTIDGKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVTIDGKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFE 319

RESULT 15

US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03

; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3
Query Match 97.9%; Score 903; DB 4; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVTIDGKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVTIDGKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFE 319

Search completed: January 13, 2005, 15:34:35
Job time : 9.50625 secs

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